

Tue Apr 20 10:02:30 2004

us-09-508-377-12.rst

Page 1

GenCore version 5.1.6
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OK protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 19:51:10 ; Search time 3340 Seconds

(without alignments)
6866.513 Million cell updates/sec

Title: US-09-508-377-12
Perfect score: 4169
Sequence: 1 MATRAVSATIGVAPPA.....PSFSYTPSRVAVYALTE 768

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_p2n.model -DEV=xlh
-O=/cgn2.1/USPTD-SPool/US09508377/runat.150422004.084306_2316/app_query.fasta.1.967
-DB=EST -QFMT=fastsp -SUFFIX=rest -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd -LIST=45
-OCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NCM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEVTIMEOUT=120 -WARM TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST: *
1: em_estba: *
2: em_esthum: *
3: em_estini: *
4: em_estmu: *
5: em_estrov: *
6: em_estrpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
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13: gb_est4: *
14: gb_est5: *
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17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vit: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rtd: *
26: em_gss_phg: *
27: em_gss_vit: *
28: gb_gss1: *

29: gb_gss2: *
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Query Length	DB ID	Description
1	3379.5	81.1	2766	11	AY109521 Zea mays
2	3150.5	75.6	2732	11	AY109532 Zea mays
3	2128	51.0	2738	11	AK009815 Mus muscu
4	2127	50.9	2862	11	AK050365 Mus muscu
5	2121	50.9	3012	11	AY105679 Zea mays
6	2054	49.3	2044	29	AY413117 Mus muscu
7	2047	49.1	2109	29	AY413115 Homo sapi
8	2002	48.0	3305	11	AK050423 Mus muscu
9	1995	47.9	2109	29	AY413116 Pan trogl
10	1412	33.9	852	14	CD438018 CD438018
11	1404	33.7	871	14	CD440241 CD440241
12	1352.5	32.4	871	14	CD444875 CD444875
13	1340	32.1	796	14	CD445867 CD445867
14	1267	30.4	801	10	BE195628 BE195628
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19	1219	29.2	690	13	CA083722 CA083722
20	1197	28.7	672	13	CA022075 CA022075
21	1197	28.7	678	9	AV939010 AV939010
22	1197	28.7	1161	14	CD505751 CD505751
23	1195	28.3	736	14	CD444184 CD444184
24	1178.5	28.3	1524	10	BE636603 BE636603
25	1159.5	27.8	695	13	BQ240494 BQ240494
26	1141	27.4	728	10	BQ008463 BQ008463
27	1138	27.3	650	10	BE427534 BE427534
28	1129	27.1	698	14	CD827444 CD827444
29	1128	27.1	623	13	BQ986883 BQ986883
30	1124	27.0	713	13	CA202517 CA202517
31	1110.5	26.6	650	10	BE602527 BE602527
32	1094.5	26.3	731	14	CB629365 CB629365
33	1093.5	26.2	831	14	CD890409 CD890409
34	1093	26.2	621	14	CD446615 CD446615
35	1090	26.1	926	14	CD446615 CD446615
36	1080	25.9	1482	28	BH770747 BH770747
37	1070	25.7	594	6	AL812505 AL812505
38	1066	25.6	592	10	BE402623 BE402623
39	1066	25.6	592	13	BQ608128 BQ608128
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43	1052	25.2	659	13	BQ588993 BQ588993
44	1051	25.2	592	12	BQ268430 BQ268430
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ALIGNMENTS

RESULT 1
AY109521
LOCUS AY109521
DEFINITION Zea mays CU1245_1 mRNA sequence.
ACCESSION AY109521
VERSION AY109521.1 GI:21213273
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 2766)

	QY	504	GluUdeuleuylsgInserAspSglIuseRlrylsMetGlyAplILeValH;EtHLeuthr	523
	Db	1637	NNNNNNNTGAAGCAAAAGTGAACGAATATTGGGAAATGGGTGCATCGTGCAACCTTAACA	1696
	QY	524	AsnAArgTrgrrTPlenGluLysCysValThrTyxAlagUserrHisAspGlAlaleuVal	543
	Db	1697	AAGAAGAGGGGGCTGAAAAGTGTGTCATTATTTGTGAAGTCAATGATCAAGCTCTTGT	1756
	QY	544	GlyAspLystrHrILealAlphaetrPleuMeCaspLysAspMetTyxAspPheMetAlaleu	563
	Db	1757	GGTAGCAAGAACAAATGCATTCGTGGTTATGATAGATATAGTATGATTTCATGGCTCTG	1816
	QY	564	AspArgProSerThrProArgILeAspArgLYLealaUdeuHsllysMetILEargIeu	583
	Db	1817	GACAGGCCCTTCAAAGCCCTCGCATCGATCGTGGAATAGCATTAACATAAATGATTAGGCTT	1876
	QY	584	ValThrMetGlyLeuGlyGlyGluNGlyTYrLeuasnPhMetGlyAsnGluPhenGlyHis	603
	Db	1877	GTCACAATGGGATTAGAGAGGAAGGCGCATTTAATTTCAAGGAAAGAAAGATTGGCGCAT	1936
	QY	604	ProGluTrpIrlleAspPheProArgGLYProlInHrIeuProtnGlyLysValIeu	623
	Db	1937	CCTGAATCGATAGATTTTCCAAAGAGGTCCTCAAAAGTCTCCAANNGGCTCGCTATCTCT	1996
	QY	624	GlyAsnAsnAsnSerTyxAspLysCyseArgArgPheAspLeuGlyAspAlasPhe	643
	Db	1997	GGGAAATACAAATAGCTTGATTAATGCGCGCGTGAATTTGACTCTGGAGATGACAGATTAT	2056
	QY	644	LeuArgTrgrrHsgILyMetGlnGluPhaspsdIALametGlnHslenGluGluTyx	663
	Db	2057	CTTAGATATCGTGGTATGCANAAGATTGGACCAGGCATGCGACCTTTGAGGAAAAATAT	2116
	QY	664	GlyPheMetHrSerGlnHsgILNtyrValserArgLysHsgILuAspLysValIle	683
	Db	2117	GAATTTCATGACATCTGATCACTCATATGATATCACGGAAGCATGAGAGAGATAGGTGATC	2176
	QY	684	IlePheGluArgGlyAspLeuValPheValPheasnPhetiSTPserAsnSerPhephe	703
	Db	2177	ATCTTTAGAGAGAGAGATTGGTCTTGCTGTCAACTTCACTGAGCAAAATAGCATATT	2236
	QY	704	AspTyxArgValGlyCySeSerArgProGlyLysTyxValAlaleuAspSerAspasp	723
	Db	2237	GACATACCGCTGGCTTGTTCACGCTCGGAGACAGACATCGTTTAGATTCGACGAT	2296
	QY	724	AlaleuPheGlyGlyPheSerArgLeuAspHisAspValAspTyxPheTh-Th-GluHis	743
	Db	2297	GGCCTTTTCGGTGGATTAGTCGGCTTGATCATGATGCTGATCTTCACGCTGACCTGG	2356
	QY	744	ProHisAspAsnaAgProArGserPheSerValTyxThrProSarArgThAlaVal	763
	Db	2357	CCGATACACAAACAGCCCGTGTCTTTCTCGATCTATGACCCACGACAAACCCGTGCTA	2416
	QY	764	TyrAla 765	
	Db	2417	TATGCA 2422	
	RESULT 2			
	LOCUS	AY109532	2732 bp	mRNA linear HTC 17-OCT-2002
	DEFINITION	Zea mays CL1742_1 mRNA sequence.		
	ACCESSION	AY109532.1		
	VERSION	AY109532.1 GI:21213287		
	KEYWORDS	HTC.		
	SOURCE	Zea mays		
	ORGANISM	Zea mays		
	REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	AUTHORS	Spermatophytas; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD		
		clade; Panicoidae; Andropogoneae; Zea.		
		1.(bases 1 to 2732)		
		Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitelst,L.M.S.,		
		Atzner,L.W., Hanafey,M., Mozanec,M. and Tingey,S.V.		
		Mature Mapping Project/Dupont Consensus Sequences for Design of		
	TITLE			

JOURNAL	Overgo Probes
REFERENCE	Unpublished (2002)
AUTHORS	2 (bases 1 to 2732)
TITLE	Coe, E. H.
JOURNAL	Direct Submission
COMMENT	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizemap.org/ZmDB , www.zmdb.iastate.edu , www.tigr.org , or NCBI, www.ncbi.nlm.nih.gov . When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu .
FEATURES	Location/Qualifiers
Source	1..2732
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	/mol_type="mRNA"
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	/db_xref="taxon:457"
	/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
ORIGIN	
Alignment Scores:	
Prod. No.:	0
Score:	3150.50
Percent Similarity:	82.96%
Best Local Similarity:	75.55%
Query Match:	75.57%
DB:	11
US-09-508-377-12 (1-768) x AY109532 (1-2732)	
Qy	2 AlatrhrpheaIaValserGIyAlatrhrheugIyValaIaArpProBrOaIaIaIaA--- 20
Db	278 GCGGTCATGGTTCCGAGAGGCGAGATATGAGCTCGATCAAGGGCTGCTGGCTCAA 337
Qy	21 ---GlnProgluGluLeuGlnIleProgluAapIleGluGlnIthrAlaGluValasn 39
Db	338 TTCAGTCGGATGGAATCGAGGTACCA--GACATTTCGAAGAACA----- 362
Qy	40 MetthrGIyGlyThrAlaGluLeuGluIuserSerGIuProThrGlnGlyIleValGlu 59
Db	382 ----- 362
Qy	60 ThrIleThrAspGIyValThrIleGIyValIysGluLeuValaIaGlyGluIysProArg 79
Db	383 -----ACGTGCGGTGCT-----GGTGTGGCTGATGTCTCAAGCCTTGAACAGAGTTGCA 430
Qy	80 ValValAlProIysProGIyAspGIyGlnIysIleTyrgIuIleAspProThrIleuIysAsp 99
Db	431 GTGGTNNNNNNNACCAAGCATGAGACNNNNNNNTATTCAGATTGACCCCATGTTCACAGGC 450
Qy	100 PheaTserSerIleuAspTyraGtyrSerGIuTyraGargIleArgIaIaIaIeAsp 119
Db	491 TATAAGTACCATCTTGAGTATCGGTACAGCCCTCTATGAAGAATCCGTTCCAGACATTGAT 550
Qy	120 GlnIleGIuGIyGlyLeuGIuAlaIaPheSerArgGlyTyrgIuIleuGIyPheThrArg 139
Db	551 GAACATGAGAGAGGCTTGGAAGCCCTCCCGGTATTTGAAGAAGTTTGATTTAATCCG 610
Qy	140 SerIaGIuGIyIleThrTyraGArgIuThrAlaProGIyAlaIaIeSerIaIaIeVal 159
Db	611 AGCGCGAAGGTATCACATATCGAAGATGGGCTCTTGAGCATTTTCTCGACGATTGGTG 670
Qy	160 GlyAspPheaIaValAspIleProIasnProIasnIaAspIleMetIleThrArgAspTyrgIyVal 179

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DB 671 GGTGACCTTCAACACATGGATCCAAATGCAAGATCGTATGAGCANNNNNTGANNNNNNNNNN 730
QY 180 TSPGUILLEPheLeuProAsnAlaAspGlySerProAlaIleProHisGlySerArg 199
DB 731 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 790
QY 200 ValIysIleArgMetAspThrProSerGlyValIysAspSerIleSerAlaTrpIleLys 219
DB 791 GTAAAGGTGAGATGATGATCTCATGAGGATTAAGATTTCAATTCAGCTGGATGATGAG 850
QY 220 PheSerValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProGlu 239
DB 851 TACTAGTCCAGGCCCGACGAAATACATAGATGAGGATTTATATATATATCTCTCTGA 910
QY 240 GluGluValTyrValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyr 259
DB 911 GAGGTAAAGTATGCTGTTCAGGATGCGCAACCTAAACGCAAAATCATTTGCGATATAT 970
QY 260 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArg 279
DB 971 GAAACACATGTCGAGATGATGAGCCCGGAACCGAATTAANNNNNNNNNNNNNNNNNN 1030
QY 280 AspGluValIleuProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIle 299
DB 1031 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1090
QY 300 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSer 319
DB 1091 CAAGAGCACTCATATATATGAGAGCTTTGGATACCATGTAATAANNNNNNNNNNNNNNNN 1150
QY 320 SerArgPheGlyThrProGluAspLeuLysSerIleLeuAspArgAlaHisGluLeuGly 339
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QY 340 LeuLeuValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeu 359
DB 1211 TTGCTAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1270
QY 360 AsnGlyPheAspGlyThrAspThrHisTyrPheHisGlyValProArgGlyHisIleTrp 379
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QY 380 MetTrpAspSerArgLeuPheAsnThrArgLysSerTrpGluValLeuArgPheLeuLeuSer 399
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QY 400 AsnAlaArgTrpTrpLeuGluLysTyrLysPheAspGlyPheArgPheAspGlyValThr 419
DB 1391 AATGCTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1450
QY 420 SerMetMetTyrThrHisIleGlyLeuGlnMetThrPheThrGlyAsnTyrGlyLysTyr 439
DB 1451 TCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1510
QY 440 PheGlyPheAlaThrAspValAspAlaValIleTyrLeuMetLeuValAsnAspLeuIle 459
DB 1511 TTGCTTGTTCACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1570
QY 460 HisGlyLeuHisProAspAlaValSerIleGlyLysPheValSerGlyMetProThrPhe 479
DB 1571 CATGACCTTATTCCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1630
QY 480 CysIleProValProAspGlyValGlyPheAspTyrArgLeuHisMetAlaValAla 499
DB 1631 GCCCTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1690
QY 500 AspLysTrpIleGluLeuLysGlnSerAspGluSerTrpLysMetGlyAspIleVal 519
DB 1691 GACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1750
QY 520 HistTrpLeuThrAsnArgTrpTrpLeuGluLysCysValThrTyrAlaIleSerHisAsp 539

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QY 540 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 559
DB 1811 CAGCATTTGTCGGGACACAGACTATTTGGCTTTGGTGTATGACACAGGATATGATGAT 1870
QY 560 PheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLys 579
DB 1871 TTCATGCGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1930
QY 580 MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnMetGlyAsn 599
DB 1931 ATGATTAGCTTATACCAATGAGGATTTAGAGAGAGGAGGATCTTAAATTTCAATGGA 1990
QY 600 GluPheGlyHisProGluTrpTrpIleAspPheProArgGlyProGlnThrLeuProThrGly 619
DB 1991 GAGTTTGACATCCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2050
QY 620 LysValLeuProGlyAspAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGly 639
DB 2051 AAGTTTATTCAGGAGAAATACAAAGATTATGACAAATGCGTGAAGATTTGACCTGGGT 2110
QY 640 AspAlaAspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeu 659
DB 2111 GATCAGACTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2170
QY 660 GluGluLysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGluGlu 679
DB 2171 GAGCANNNNNTATGAATTTCACTGATGATGATGATGATGATGATGATGATGATGATG 2230
QY 680 AspLysValIleIlePheGluArgGlyAspLeuValPheAsnMetHisIleTrpSer 699
DB 2231 GATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2290
QY 700 AsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeu 719
DB 2291 AACACGATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2350
QY 720 AspSerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTrpPhe 739
DB 2351 GACTCCGAGCGTGAATATTTGATGATGATGATGATGATGATGATGATGATGATGATG 2410
QY 740 ThrTrpGluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArg 759
DB 2411 ACCGCCAGCTGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2470
QY 760 ThrAlaValAlaTyrAlaLeuThrGlu 768
DB 2471 ACATGTGTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2497

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RESULT 3
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 LOCUS AK009815
 DEFINITION Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310045H19 product:glucan (1,4-alpha-), branching enzyme 1, full insert sequence.
 ACCESSION AK009815.1 GI:12844841
 VERSION AK009815
 KEYWORDS HTC; CAP trapper
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2
 Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, N. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to

Db	444	CTGAAGGAGTATTATTA	CTAGTAAGAGTGGCCAGATACCTGTTATCCCATTTTCCCATGGGCA	503
Qy	219	LysPheSerValGlnAlaProGlyIle	LeProPheAsnGlyIleTyrTyrAspProPro	238
Db	504	AAGTATGTCGTTCCGTAGAGAACAAACACGTGAACATGATGTGATACATCTGGGGCTCA	---	560
Qy	239	GluIleGluIuIyIyValPheGlnHisProIle	ProIuIyAsnArgProGluSerLeuAlaGle	258
Db	561	---GAGAGCCCCCTTAATTAATTAAGCATTTCCAGCTTAAGAAACCAAGAGCGTTAAGATT		617
Qy	259	TyrGluSerHisIleGlyMetSerSerProGluProIyIleAsnSerTyrAlaAsn	Phe	278
Db	618	TATGATATCTATCTATGGGAAATTTCTTCCACAGAAAGAAAATAGCTTCTTACAAACATTTT		677
Qy	279	ArgAspGluValLeuProArgIleIleYAsnGluGlyTyrAsnAlaValGlnIleMetAla		298
Db	678	ACCAAGCAATGACTACCAACAGATCAAGACCTTGGGTATTACTCATCATCACTGATGATGCG		737
Qy	299	IleGlnGlnHisSerTyrTyrAlaSerPheGlyTyrHisValIle	ThrAsnPhePheAlaPro	318
Db	738	ATCATGGAACATGCTTACTATATGCCAGTTTGGGTACCAATACAGAGCTTTTTCGACCT		797
Qy	319	SerSerArgPheGlyThrProGluAspLeuSerLeuIleAspArgAlaHisGlu	Ileu	338
Db	798	TCAAAGTCGTATGGAACCTCGGAAGACTGMAAAGACTTGTGACACAGCCATTTCCATG		857
Qy	339	GlyLeuLeuValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGly		358
Db	858	GGCATTTGATGCTCCCTGATGCTGGTTCATAGCCATGCTTCAAAAATATTCAGAAAGATGGG		917
Qy	359	LeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisHis		378
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Qy	379	TrpMetTrpAspSerArgLeuPheAsnTyrGlySerTrpGluValIleArgPheLeu	Ileu	398
Db	978	GATCTTGGACAGTAAATTATTTATCTATTCACAGCTGGAAAGTTTAAGATTCCTTCTG		1037
Qy	399	SerAsnAlaArgTrpLeuGluGlnIuTyrLysPheAspGlyPheArgPheAspGlyVal		418
Db	1038	TCGAACATTAATGCTGGTGGAGAGTAACTGCTTGAATGCTCCGTTTGAAGGATGTC		1097
Qy	419	ThrSerMetMetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGlu		438
Db	1098	ACCTTATGCTCTCATCATCACACAGGAATGGGTCAAGGTTTTCGGGTACCTAATAAGAA		1157
Qy	439	TyrPheGlyPheAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAsp	Ileu	458
Db	1158	TATTTGGACTACCAAGTAAATGAAATGCTTGAATTTATCTCAATGTTGGCAATCATTTG		1217
Qy	459	IleHisGlyLeuHisProAspAlaValSerIleGlyIuAspValSerGlyMetProThr		478
Db	1218	GCTCACACGTTGTTACCAAGCTCCGATTAACATAGACAGAGATGTTACGGAGTCCGGCT		1277
Qy	479	PheCysIleProValProAspGlyGlyValGlyPheAspTyrArgLeuHisMetAlaVal		498
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Qy	499	AlaAspIyIyTrpIleGluLeuLeuLysGln---	SerAspGluSerTrpIyMetClyAsp	517
Db	1338	CCAGTAAATGATGCCAATTAATTAAAGATTAAAGATGAAGCTGGAATATGGGCAT		1397
Qy	518	IleValHisThrLeuThrAsnArgArgTrpLeuGluIuIyCysValThrTyrAlaGluSer		537
Db	1398	ATAGTGTATCTCTACCAATGACATGACGCTACCTTGAAAAATGTGTGGCTTATGACAGAGGT		1457
Qy	538	HisAspGlnAlaLeuValGlyAspIyThrIleAlaPheTrpLeuMetAspIyAsnMet		557
Db	1458	CATGATCAGGCAATGTGGTGTGACAAAGACACTGGCGTTTGGTGTATGACCGCTGAGATG		1517
Qy	558	TyrAspPheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeu		577

Db		1518	TACACGAACAATGAGCGCTTGCCGCCCTTTCACCTCAGTAATTGATCGAGGANAACAGCTT	1577
Oy		578	HistylemettleaagilevalThmmeqlyleuglyglvluuglytyrleuanpheMet	597
Db		1578	CATAAGATGATGCCTCATCACTCACGGCTCGTGTGAAGAAGGCTATCTCAATTTATG	1637
Oy		598	GlyasniguphegiHisProglutridlaspPheproargglyProginthrLeupro	617
Db		1638	GGTAATGAGTTTGGGACTCTCGAATGGTTGGACTTCCAAAG-----	1679
Oy		618	ThrilyValleuProglyAsnaasnaseryTyrsaplyscysariga-glpneasp	637
Db		1680	-----AAGGAAATAAGAGATTACCATTATGCCAGNAGAGATTATAT	1724
Oy		638	LeucliyaspaLaaspphleueuarxyrhiisgylmecInglupheasrglnalamerGl	657
Db		1725	TTAACCGACGATGACTCTTCCTCGTATTAAGTCTCTTAATAATCTTGACAGATATGAAT	1784
Oy		658	HisteuglugulystyryglyPheMetThrsedgluhisglntryValserArgLyshis	677
Db		1785	AGACTGGAGAAATATGTGTGCTTCCTTCAGCTCCAAGGCTACGTGAATGAAAAAT	1844
Oy		678	GlulugluplyValillelelephegiuargglyaspIeuvalPhevalPheasnPhehis	697
Db		1845	GAAACCAATAGAACAATACACTTTGAGAGAGACAGAGACTTCTTTATTTTCAAATTCCAC	1904
Oy		698	TrpseranserPhiephieaspyTYRARGVALGLYCYSERARGPROGLYLYSTYRYLVAL	717
Db		1905	CCAAAGCAAGAGCTTTACGGACTCCCGAGTGGGACACACACCGAGGAAGTTCAAAATT	1964
Oy		718	AlaleuaspsesaspaspaLaLeuPheglVglyPheseraArgleuasPHisasPvalasp	737
Db		1965	GTTACTAGATTGTGCGCAGCGAGATATGAGGTATATAGAGACTGACCCACACACCAAC	2024
Oy		738	TyrPheThrThrgluHisProHisaspAsnArgProArgrSerPheSerValIlyrTh-Pro	757
Db		2025	TACTTTGGTAGCGCTTTGAAACATAATATGGGGCCCCCTATCTCTTGCTGATCATTTCCA	2084
Oy		758	SerArgThrAlaValVal 763	
Db		2085	AGCCGAGTGCCTCTCATC 2102	
RESULT 4				
AKO50365		2862 bp	mRNA	linear HTC 20-SEP-2003
LOCUS				
DEFINITION		Mus musculus adult male liver tumor cDNA, RIKEN full-length		
		enriched library, clone:C730040P17 product:glucan (1,4-alpha),		
		branching enzyme 1, full insert sequence.		
AKO50365				
ACCESSION		AKO50365.1 GI:26341095		
VERSION				
KEYWORDS		HTC; CAP trapper.		
SOURCE		Mus musculus (house mouse)		
ORGANISM		Mus musculus		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE				
AUTHORS		1 Carninci,P. and Hayashizaki,Y.		
TITLE		High-efficiency full-length cDNA-cloning		
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE		99279253		
PUBMED		10349636		
REFERENCE				
AUTHORS		2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,		
TITLE		Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
JOURNAL		Normalization and subtraction of cap-trapper-selected cDNAs to		
MEDLINE		prepare full-length cDNA libraries for rapid discovery of new genes		
PUBMED		Genome Res. 10 (10), 1617-1630 (2000)		
REFERENCE				
AUTHORS		3 Shimbata,K., Itoh,M., Aizawa,K., Nagosaka,S., Sasaki,N., Carninci,P.,		
TITLE		Kono,H., Akiyama,U., Nishi,K., Kibunai,T., Tashiro,H., Itoh,M.,		
JOURNAL		Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,		
MEDLINE		11042159		
PUBMED		20499374		
REFERENCE				
AUTHORS				

JOURNAL	Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Taniuchi, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN Integrated Sequence Analysis (RISA) system--384-format
REFERENCE	Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL	20530913
MEDLINE	
REFERENCE	11076861
AUTHORS	4
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
JOURNAL	Functional annotation of a full-length mouse cDNA collection
REFERENCE	Nature 409, 685-690 (2001)
TITLE	5
JOURNAL	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
REFERENCE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
AUTHORS	Nature 420, 563-573 (2002)
TITLE	6 (bases 1 to 2862)
JOURNAL	Aachi, J., Aizawa, K., Akimura, T., Arai, T., Bono, H., Carninci, P.,
REFERENCE	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
AUTHORS	Hayashida, K., Hayatsu, N., Hizemoto, K., Hiraoka, T., Hirozane, T.,
TITLE	Kochi, F., Imochi, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
JOURNAL	Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M.,
REFERENCE	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
AUTHORS	Nakamura, Y., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N.,
TITLE	Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
JOURNAL	Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
REFERENCE	Sojabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S.,
AUTHORS	Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
TITLE	Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Direct Submission
REFERENCE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
AUTHORS	Physical and Chemical Research (RIKEN), Laboratory for Genome
TITLE	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
JOURNAL	RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama,
REFERENCE	Kanagawa 230-0045, Japan (E-mail: genome-resesgcs.riken.go.jp,
AUTHORS	URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
TITLE	Fax: 81-45-503-9216)
JOURNAL	CDNA library was prepared and sequenced in Mouse Genome
REFERENCE	Encyclopedia Project of Genome Exploration Research Group in Riken
AUTHORS	Genomic Sciences Center and Genome Science Laboratory in Riken.
TITLE	Division of Experimental Animal Research in Riken contributed to
JOURNAL	prepare mouse tissues.
REFERENCE	Tissue was provided by William A. Held, Roswell Park Cancer
AUTHORS	Institute, Department of Molecular and Cellular Biology, Elm and
TITLE	Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully
JOURNAL	acknowledge.
REFERENCE	Please visit our web site for further details.
AUTHORS	URL: http://genome.gsc.riken.go.jp/.
TITLE	URL: http://fantom.gsc.riken.go.jp/.
JOURNAL	Location/Qualifiers
REFERENCE	1..2862
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AUTHORS	92..2200
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JOURNAL	branching enzyme I (MGB MGI:1921435, GB NM_028803,
REFERENCE	branching enzyme I (MGB MGI:1921435, GB NM_028803),
AUTHORS	putative"

[illegible]

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DEFINITION        Zea mays AY105679
ACCESSION         AY105679
VERSION           AY105679.1 GI:21208757
KEYWORDS           HTC
SOURCE            Zea mays
ORGANISM          Zea mays
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                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE          1 (bases 1 to 3012)
AUTHORS           Kainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S.,
                  Arthur,L.W., Hanafey,M., MORGANTE,M. and TINGEY,S.V.
TITLE             Maize Mapping Project/Dupont Consensus Sequences for Design of
                  Overgo Probes
JOURNAL            Unpublished (2002)
REFERENCE          2 (bases 1 to 3012)
AUTHORS           Coe,E.H.
TITLE             Direct Submission
COMMENT           Submitted (25-APR-2002) Maize Mapping Project, University of
                  Missouri, Columbia, MO 65211, USA
                  If you are interested in getting corresponding physical clones,
                  these are publicly available in getting from ZmDB and may be found by BLAST
                  searching at MSI, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
                  www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
                  maize cDNA sequences is either Virginia Walbot, Stanford or Pat
                  Schnable, Iowa State, then clones may be requested from ZmDB:
                  www.zmdb.iastate.edu.
FEATURES          location/Qualifiers
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                    /clone_lib="Maize Mapping Project/Dupont Consensus
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                    /note="this sequence is part of a project of EST
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                    configs to seed Dupont configs; this resource was
                    assembled by Dupont as part of a collaboration for the
                    overgo addressing of BACs in conjunction with the Maize
                    Mapping Project"
ORIGIN
Alignment Scores:
Pred. No.:      3,71e-226      Length:      3012
Score:          2121.00      Matches:      393
Percent Similarity: 71.18%      Conservative: 101
Best Local Similarity: 56.63%      Mismatches:  173
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DB: 11 Gaps: 6

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 RESULT 6
 AT413117

QY 367 ThrHiEtYrPheHiEgLYgLYProARgLYHiHiEtYrMetYrPaSPSeArXLeuPhe 386
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REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCES
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
2
10349636
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, Y., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
3
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Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Komno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,
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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
4
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The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3305)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
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Takekida, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
Direct Submission
16 JUN 2001 Yeshibide Hayashizaki The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-ku, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge.

Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>.

FEATURES

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Best Local Similarity: 58.10%      Mismatches: 151
Query Match:      48.02%      Indels:      16
DB:              11      Gaps:      5
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ORIGIN

Alignment Scores:

Pred. No.: 1.05e-212 Length: 3305
Score: 2002.00 Matches: 366
Percent Similarity: 73.49% Conservative: 97
Best Local Similarity: 58.10% Mismatches: 151
Query Match: 48.02% Indels: 16
DB: 11 Gaps: 5

US-09-508-377-12 (1-768) x AK050423 (1-3305)

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 REFERENCE 1 (bases 1 to 2109)
 AUTHOR Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.O.,
 Adams,M.D. and Cargill,M.
 TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous
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 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 2109)
 AUTHOR Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.O.,
 Adams,M.D. and Cargill,M.
 DIRECT SUBMISSION

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
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              190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
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 VERSION CD440241.1 GI:31355884
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE
 AUTHORS Zukaroyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 881)
 Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
 Messing, J.
 Sequencing of the maize endospERM ESTs
 Unpublished (2002)
 CONTACT
 Contact: Lai, Jinsheng
 Dr. Joachim Messing's Lab
 Waksman Institute, Rutgers University
 190 Freilighuysen Rd., Piscataway, NJ 08854, USA
 Tel: 732-445-3801
 Fax: 732-445-5735
 Email: jlai@waksman.rutgers.edu
 Seq primer: T3.

FEATURES
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US-09-508-377-12 (1-768) x CD440241 (1-881)

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Tue Apr 20 10:02:30 2004

us-09-508-377-12.rst

Page 20

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QY 252 ArgProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProIys 271
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 21:39:56 ; Search time 579 Seconds
(without alignments)
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Title: US-09-508-377-12

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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34	1967.5	47.2	3753	12	US-10-239-145-6	Sequence 6, Appli
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APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequr Rahman
TITLE OF INVENTION: Baitly with altered branching enzyme activity and starch and sta
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434.893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 2.1
SEQ ID NO 1
LENGTH: 2554
TYPE: DNA
ORGANISM: Hordeum vulgare
FEATURE:
OTHER INFORMATION: SSBEITA CDNA
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US-09-508-377-12 (1-768) x US-10-434-893A-1 (1-2554)

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Db      2044 AAGTACCAAGGTCGCTTACCTGATGATGCACTTTGGTGGATTCAGCAGGCTTGAT 2103
Qy      734  HisAPValAspTyrPheThrThrgluHisProHisAspAsnArgProArgSerPheSer 753
Db      2104 CATGATGTCGACTACTTCACAACCGAACATCCGCAATGACACAGGCGCAGCTCTTCTCG 2163
Qy      754  ValTyrThrProSerArgThrAlaValAlaTyrAlaLeuThrGlu 768
Db      2164 GTGTACACTCCGACGACGAACCTGGGTCGTGTATGCTTACCTTACAGAG 2208

RESULT 2
US-09-792-127-3
; Sequence 3, Application US/09792127
; Patent No. US2002002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Search Branching Enzyme IIB
; FILE REFERENCE: B81439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Triticum aestivum
; US-09-792-127-3

Alignment Scores:
Pred. No.: 0 Length: 3039
Score: 3363.00 Matches: 607
Percent Similarity: 89.27% Conservative: 75
Best Local Similarity: 79.45% Mismatches: 68
Query Match: 80.67% Indels: 14
Gaps: 4
DB: 9

US-09-508-377-12 (1-768) x US-09-792-127-3 (1-3039)
Qy      7  SerGIyAlaThrLeuGIyValAlaArgProAlaAlaAlaGlnPro----- 22
Db      294 AGTGGCGGAACA-----CCGCTTCCATCGACGGTCCCGTTCAGTTGAT 338
Qy      23  ---GluGluLeuGlnLeuProGluAspIleGluGlnThrAlaGluValAsnMetThr 41
Db      339 TCTGATGATCTGAAAGGTTCCA---TTCATGATGATGAACA-----AGCTTACAG 386
Qy      42  GluGIyThAlaGluLysLeuGlnUserSerGluProThrGlnGluIleValGluThIle 61
Db      387 GATGGAGGTGAAGATAGTATTGGTCTTCAGACCAATCAGGTACTGAAGAATTGAT 446
Qy      62  ThrAspGIyValThrIySGIyValIySGIyLeuValAlaGIyGluLysProArgValAla 81
Db      447 GCTGAAGACACGACGACGAATGACAAAGAAATCATCTCGACGAGGAATTAACGATTCTG 506
Qy      82  ProLysProGIyAspGIyGlnLysIleTyrGlnIleAspProThrLeuLysAspPheArg 101
Db      507 CCACCAACCGGAAATGACACGAAATATACAGATTGACCAACGCTCCGAGACTTTAAG 566
Qy      102  SerHisLeuAspIyArgTyrSerGluTyrArgArgIleArgAlaIleAspGlnHis 121
Db      567 TACCACTCTTGAGTATGATATAGCTATACAGGAAATACGTTAGACATTGATGAACAC 626
Qy      122  GluGIyGIyLeuGluAlaPheSerArgIyTyrGIyLysLeuGIyPheThrArgSerAla 141
Db      627 GAAGGAGGCAATGATATTTTCCCGCGGTTACGAGAAGTTTGATTATGCGCAGCGCT 686
Qy      142  GluGIyIleThrTyrArgGluTyrAlaProGIyAlaHisSerAlaAlaLeuValGIyAsp 161

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Db      1767  TGGATTGGAACCTTCTCGAAGGAAAGCAATGAAGCTTTGGAGATGGGTAAATTATTTGTCACACCA 1826
QY      522  LeuthraenaArgArgTyrPleuGluLysCysValThrTyrAlaGluSerHisAspGlnAla 541
Db      1827  CTAACAAACAGAAAGGCTGCTGGAAAAGTGTGTACTTAATCTGTAAGCTCAGATCAAGCA 1886
QY      542  LeuValGlyAspPheThrIleAlaPheThrPheMetSerAspLysAspMetTyrAspPheMet 561
Db      1887  CTTGTGGAGACAAAGACTATTTGCAATCTGTTGATGGACAAAGATATGATGATTTCACTG 1946
QY      562  AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMetIle 581
Db      1947  GCGCTGAACGGACCTTCGACGCGCTAATATGATCGTGAATAGCAGTGCATTAATAATGATT 2006
QY      582  ArgLeuValThrMetGlyLysGlyGlyGlyGlyTyrIleLeuSerPheMetGlyAsnGluPhe 601
Db      2007  AGACTTATCAACAATGGTCTGTAGAGAGAGAGGGTATATCTTAACCTTAATGGGAAATGAGTTC 2066
QY      602  GlyHisProGluThrIleAspPheProArgGlyProGlnThrLeuProThrGlyLysVal 621
Db      2067  GGGCAATCCTGAATGGATAGTAACTTTCCAAAGGCCCAAGACTCTCCAAAGTGTTAGTTC 2126
QY      622  LeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 641
Db      2127  ATCCCAAGAAACAACAACAGTTACGACAAATGCGCTGGAAGATTGACCTGGGTATGCA 2186
QY      642  AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
Db      2187  GAATTTCTTAGGTATCATGGTATGACAGAGTTGATGATGACGCAAGACAGCATCTTGAGAA 2246
QY      662  LysTyrGlyPheMetThrSerGluHisGlnTyrValSerArgLysHisGluGluAspLys 681
Db      2247  AATATTCGTTTATATGCAATCAAGACCAACCACTACTCTCGGAAACATGAGGAAATAG 2306
QY      682  ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTyrSerAsnSer 701
Db      2307  GTGATCGTGTGTGAAAAAAGGGGACTTGGTATTGTGTCAACTTCACCTGAGTGATGAC 2366
QY      702  PhePheAspTyrArgValGlyCysSerArgProGluLysTyrValAlaLeuAspSer 721
Db      2367  TATTTGACTACCGGGTGGCTGTTAAAGCTGGGAAGTCAAGTGTCTTAAGCTCG 2426
QY      722  AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741
Db      2427  CACGCTGGACTCTTTGGTGAATTTGGTAGATTCATCACTGACGAGACAGCTCACTTCT 2486
QY      742  GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761
Db      2487  GACTGCCAATGATGACAAACAGGCCCATTCATTCTCAGTGTCACACTCTTAAGCAAGAACTGT 2546
QY      762  ValValTyrAla 765
Db      2547  GTTGTCTATGCT 2558

RESULT 3
US-10-434-893A-2
; Sequence 2, Application US/10434893A
; Publication No. US20040060083A1
; GENERAL INFORMATION:
; APPLICANT: Ahmed Regina
; APPLICANT: Matthew Kennedy Morell
; APPLICANT: Sadequr Rahman
; TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and
; TITLE OF INVENTION: containing products with an increased amylose content
; FILE REFERENCE: 69425
; CURRENT APPLICATION NUMBER: US/10/434, 893A
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO: 2
; LENGTH: 2780
; TYPE: DNA

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: FEATURE:
: OTHER INFORMATION: SSBEIIB CDNA
US-10-434-893A-2

Alignment Scores:
Pred. No.: 0 Length: 2780
Score: 3348.50 Matches: 605
Percent Similarity: 88.50% Conservative: 72
Best Local Similarity: 79.08% Mismatches: 75
Query Match: 80.32% Indels: 13
DB: 12 Gaps: 3

US-09-508-377-12 (1-768) x US-10-434-893A-2 (1-2780)

QY      8  G|V|A|I|A|T|H|L|E|U|G|I|V|A|I|A|A|A|P|R|O|P|R|O|A|I|A|A|A|-----G|N|P|R|O      22
Db      208 GGGCGTAGTGGCGGAGGAGGAGAACCCGCTTCCATCCAGGAGGTTCCGTTCAAGTTCAGGTGCT      267
QY      23  G|U|G|U|E|U|G|I|N|I|E|P|R|O|-----G|U|A|P|I|E|G|U|G|I|N|I|T|H|A|G|I|U|A|I|S|E|N|E|C      40
Db      268 GATGATCTGAGAGGCTTCCATTCATCCAGCAT-----GAAACCAGACCTG      309
QY      41  T|H|G|I|G|Y|I|N|T|A|G|I|U|L|E|U|L|U|B|E|U|S|E|R|G|U|P|R|O|T|H|G|I|N|G|Y|I|T|E|V|A|G|I|U|T|H|R      60
Db      310 CACGATGAGAGGTGAAGATACCTATTCGGCTTGAAGACATATACGTTACGTAAGAAAT      369
QY      61  I|L|E|T|H|A|S|P|G|I|V|A|I|T|H|L|E|S|G|Y|V|A|I|Y|A|I|S|G|I|U|E|U|A|I|G|Y|I|U|L|U|B|E|P|R|O|A|R|G|V|A|I      80
Db      370 GATGCTGAAGCGGTGACGACGAGATGAGCAAAAGATATCCACGSGTGAAGAAATACGCAAT      429
QY      81  V|A|I|P|R|O|L|Y|S|P|R|O|G|I|Y|A|S|P|G|Y|G|I|N|I|S|I|E|Y|T|G|U|I|L|E|A|S|P|R|O|T|H|R|E|U|L|Y|S|A|P|R|H|E      100
Db      430 GTGCCACAACCCGGAGAAATGAGCAGCAAAATATACGATTCGATGACCACATGCTCGAGACTT      489
QY      101 A|R|G|S|E|R|H|I|S|E|U|A|S|P|T|Y|R|A|R|G|T|Y|R|S|E|R|G|U|T|Y|R|A|R|G|I|L|E|A|R|G|A|I|A|I|L|E|A|S|P|G|I|N      120
Db      490 AAGTACCACTTGAGATCGATACAGCCCTATTTAGGAAATACGTTCAAGCATTTAGGA      549
QY      121 H|I|S|G|I|G|Y|G|Y|L|E|U|G|I|U|A|I|A|P|H|E|S|E|R|A|R|G|I|Y|T|G|I|U|L|U|B|E|U|G|Y|P|H|E|R|H|A|R|G|S|E|R      140
Db      550 TACGATGAGAGCGATGAGATGATATTTCCCGCGCTACGAGAAGTTGATTTGTTCCGACG      609
QY      141 A|A|G|I|U|G|Y|I|L|E|T|H|T|Y|R|A|R|G|U|T|P|R|A|P|R|O|G|Y|A|I|H|I|S|E|R|H|A|I|A|E|U|V|A|I|G|Y      160
Db      610 GGTGAAGGATATCACTTACCGAGAAATGGGCTCTCGAGCATTCGACACTTAAAGTTGG      669
QY      161 A|A|P|H|E|A|S|A|S|T|T|A|S|P|R|O|A|S|N|A|I|A|S|P|R|I|E|R|T|H|A|R|G|A|S|P|I|Y|G|Y|V|A|I|T|R      180
Db      670 GACTTCAACATTTGGGATCCACTGACAGCCCATATGACGCAAAATATGACTTTGG      729
QY      181 G|U|I|L|E|P|H|E|U|P|R|O|A|S|N|A|I|A|S|P|G|Y|S|R|P|R|O|A|I|L|E|P|R|O|I|S|G|Y|S|R|A|R|G|V|A|I      200
Db      730 GAGATTTTTCCTCCAAACATGAGATGGTTGGCCGCCCAATTCCTCATGGCTCACGGGTG      789
QY      201 L|Y|S|I|E|A|R|M|E|R|A|S|P|T|H|R|P|R|O|S|E|R|G|Y|V|A|I|Y|S|A|P|R|S|E|R|I|L|E|S|R|H|A|T|P|I|L|E|Y|S|P|H|E      220
Db      790 AAGGTGCGGATGATACCTCCATCTGGGACAAAGGATTCATTCCTCTTGATCAACAGTAC      849
QY      221 S|E|R|V|A|I|G|H|A|P|R|O|G|Y|G|I|U|L|E|P|R|O|P|H|E|A|S|G|Y|I|L|E|T|Y|R|A|S|P|R|P|R|O|G|I|U|G|I|N      240
Db      850 TCCGTCAACACTCCAGGAGATATACCATACATGAAATATATATATATATACCTCTGGAAG      909
QY      241 G|I|U|Y|S|T|Y|R|V|A|P|H|E|G|I|N|H|I|S|P|R|O|G|I|N|P|R|O|L|Y|S|A|R|G|P|R|O|G|I|U|S|E|R|I|E|U|A|R|G|I|E|Y|T|G|I|U      260
Db      910 GAGAAATATGTATTCACAGCATCCTCAACCTAAACGACCAAAATCATTTGCGGATATAGAA      965
QY      261 S|E|R|H|I|I|G|Y|M|E|R|S|E|R|P|R|O|G|I|U|P|R|O|L|Y|I|A|S|N|S|E|R|Y|R|A|I|A|S|N|P|H|E|R|A|R|G|A|S|P      280
Db      970 ACACATGTTGGCATGATGAGCCCGGAAACCAAGATCAACATATGCAATTCGAACTCAGGAT      1020
QY      281 G|I|U|V|A|I|E|P|R|O|R|G|I|L|E|Y|S|A|R|G|E|U|G|Y|T|Y|R|A|S|N|A|I|A|G|I|N|I|E|M|E|R|A|I|I|E|G|I|N      300
Db      1030 GCTCTCTTCTTCCATTTAAATTAATTTGATTAACAGACTTCAAAATTAAGGCATATCCAA      1080

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QY 301 GIuHsSerTyxTyxAlaSerPheGlyTyxHisValThrAnpPheAlaProSerSer 320
DB 1090 GAGCATCTACTATGAGAGCTTTGGGTACACTTTCATTCATTTCTTGACCAAGTAC 1149
QY 321 ArgPheGlyThrProGluAspLeuLysSerLeuLysAspArgAlaHisGluLeuGlyLeu 340
DB 1150 CATTGGGTGCTCCCAAGATTAAATCCTTATATAGAGCTCCAGAGCTTGTTG 1209
QY 341 LeuValLeuMetSerAspLeuValHisSerHisSerSerSerSerSerSerSerSerSer 360
DB 1210 CTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1289
QY 361 GlyPheAspGlyThrAspThrHisTyxPheHisGlyGlyProArgGlyHisHisTrpMet 380
DB 1270 GATTGATGAGCAGGATACACTTACTTTCATGCGCGCTCAGCGGCGCATCTGAGATG 1329
QY 381 TrpAspSerArgLeuPheAsnTyxGlySerTrpGluValLeuArgPheLeuSerHisn 400
DB 1330 TGGGATTCGCTGCTGCTCACTAGGGAATAGAGAACTTAAAGTTCTCACTTCCAA 1389
QY 401 AlaArgTrpTrpLeuGluGluTyxLysPheAspGlyPheArgPheAspGlyValThrSer 420
DB 1390 GCAAGATGCTGCTTACAGAAATTAAGTTGATGATGATGATGATGATGATGATGAT 1449
QY 421 MetMetTyxThrHisHisGlyLeuGluMetThrPheThrGlyAsnTyxGlyGlyTyxPhe 440
DB 1450 ATGATGTATACCAACCATGATTAACAAGTACCTTTACAGGAGCTACCAATGATATTT 1509
QY 441 GlyPheAlaThrAspValAspAlaValValTyxLeuMetLeuValAsnAspLeuHis 460
DB 1510 GCGCTTCCAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
QY 461 GlyLeuHisProAspAlaValSerHisGlyGluAspValSerGlyMetProThrPheCys 480
DB 1570 GCGCTTATCCGTAAGCGCTTACTTGTGTAAGATGTATGTAAGTACCTTACATTTGCC 1629
QY 481 IleProValProAspGlyGlyValGlyPheAspTyxArgLeuHisMetAlaValAlaAsp 500
DB 1630 CTTCCTGCTCAAGTGTGCGGTGCTGTTGACATGCTTACATATAGCGCGCTGCCAT 1689
QY 501 LysTrpIleGluLeuLeuLysGlnSerAspGluSerTrpLysMetGlyAspIleValHis 520
DB 1690 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1749
QY 521 ThrLeuThrAspArgArgTrpLeuGluLysCysValThrTyxArgLysHisAspGln 540
DB 1750 AACAATAAATAAGAGGTGTGTAAGATGTGTATCTTATGCTGTAAGTCAATGATCAA 1809
QY 541 AlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyxAspPhe 560
DB 1810 GCACCTGTTGAGACAAAGATATTGATCTGTGTATGAGCAAGATATGATGATTTTC 1869
QY 561 MetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMet 580
DB 1870 ATGGCTCTGACGACCTTCGACACCTTAATATGATGCGGAAATAGACATGCAATAATG 1929
QY 581 IleArgLeuValThrMetGlyLeuGlyGlyGlyGlyTyxLeuAsnPheMetGlyAsnGlu 600
DB 1930 ATTAGCTTATCAAAAGCTTTAGAGAGAGAGGCTTATCTTATGCTTATGAGAAATGAG 1989
QY 601 PheGlyHisProGluTrpIleAspPheProArgGlyProGlnThrLeuProThrGlyLys 620
DB 1990 TTGGGCACTCTGAATGATGATCTTCCAAAGAGCCCAACAAGTATCTCCAACTGGTAAG 2049
QY 621 ValLeuProGlyLysAsnAsnSerTyxAspLysCysArgArgArgPheAspLeuGlyAsp 640
DB 2050 TTCATCCCAAGAAATACAAAGATTACAGCAAAATGCGGTGCAAGATTGACCTGGGTAT 2109
QY 641 AlaAspPheLeuArgTyxHisGlyMetGlnLysPheAspGlnAlaMetGlnHisLeuGlu 660
DB 2110 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2169

QY 661 GluLysTrpGlyPheMetThrSerGluHisGlnTyxValSerArgLysHisGluLysAsp 680
DB 2170 GAAAAATATGCTTATATACATCAAGACCAAGTACGATCTCCGGAACACGGAAGAT 2229
QY 681 LysValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTrpSerAsn 700
DB 2230 AAGGTGATCGCTTGTGAAAAAGGACCTTGATTTGTGTTCACTTCCACTGAGATAT 2289
QY 701 SerPheAspTyxArgValGlyCysSerArgProGlyLysTrpTyxValAlaLeuAsp 720
DB 2290 AGCATTTTCGACTACCGGGTGGTTGCTTAAGCGTGGAAAGTACAAAGGTGTTAGAC 2349
QY 721 SerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyxPheThr 740
DB 2350 TCAGACGCTGACCTCTTGTGATTTGGTATGATTCATCACTGAGAGCACTTCACT 2409
QY 741 ThrGluHisProHisAspAsnArgProArgSerPheSerValTyxThrProSerArgThr 760
DB 2410 AATGCTGCCAATGATGACAAAGGCCCATTTGTTCTCACTGATCACTCTACAGAAC 2469
QY 761 AlaValValTyxAla 765
DB 2470 TGTGTTGCTATGCT 2484

RESULT 4
US-10-336-753-55
; Sequence 55, Application US/10336753
; Publication No. US2003026176A1
; GENERAL INFORMATION:
; APPLICANT: Guan, Hanping
; APPLICANT: Keeling, Peter L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; FILE REFERENCE: 2461-52
; CURRENT APPLICATION NUMBER: US/10/336,753
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/09/402,254
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 2640
; TYPE: DNA
; ORGANISM: Zea mays
US-10-336-753-55

Alignment Scores:
Pred. No.: 0 Length: 2640
Score: 3342.00 Matches: 608
Percent Similarity: 86.98% Conservative: 67
Best Local Similarity: 78.35% Mismatches: 79
Query Match: 80.16% Indels: 22
DB: 12 Gaps: 4

US-09-508-377-12 (1-768) x US-10-336-753-55 (1-2640)

QY 4 PheAlaValSerGlyAlaThrLeuGlyVal-----AlaArgProProAla 18
DB 108 TTCTTAACCTGGGAGTCTGCACTGATGATGATGATGATGATGATGATGATGATGAT 167
QY 19 AlaIaGlnProGluGluLeuGlnIleProGluAspIleGluGluGlnThrAlaGluVal 38
DB 168 GCCGCGCCAGGAAGCGGTCACTGCTTCTGAGGCGGAATAT----- 212
QY 39 AsnMetThrGlyTyxHisGlyLysLeuGluLysSerLeu----- 52
DB 213 -----GGCTCGCATCAAGGCTGACTCGGCTCAATTCACAGTCGATGAATG 260


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Db 261 GAGTACACAGACATTTCTGAAAGACAGACGTCGTGCT-----GGTGTGCTCATGCT 314
Qy 73 ValValGlyGlyLeuProArgValValProLysProGlyAspGlyGlnLysIlePheGlu 92
Db 315 CAAGCCTTGAACAGAGTTCGAGTGTCTCCCCACCACAGCATGAGCAAAAATATTCAG 374
Qy 93 IleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGlyTyrArg 112
Db 375 ATTGACCCCATGTTTGCAGGCTATAGATACCATCTTGAGTATCGGTACAGCTCATAG 434
Qy 113 ArgIleArgAlaAlaIleAspGlnHisGlyGlyLeuGlnAlaPheSerArgGlyTyr 132
Db 435 AGATCCGTCACAGCATTTGATGAACATGAGAGGCTTGGAAGCCTTCTCCGTAAGTAT 494
Qy 133 GlnLysLeuGlyPheThrArgSerAlaGlnGlyIleThrTyrArgGluTyrAlaProGly 152
Db 495 GAGAAAGTTTGATTTAATGCCAGCGCGGAGAGTATCACATTCGAAATGGGCTCTGGA 554
Qy 153 AlaHisSerAlaAlaLeuValGlyAspPheAsnAsnTyrAsnProAsnAlaAspThrMet 172
Db 555 GCATTTTCTCGACGATTCGTGGTGACCTCAACAATCGGATCCAAATGCGAGATGTATG 614
Qy 173 ThrArgAspArgTyrGlyValTyrGluIlePheLeuProAsnAsnAlaAspGlySerPro 192
Db 615 AGCAAAATAGATGTTGGTGTGGAAATTTTCTGCTTAACAATGCAATGCGATGTCATCA 674
Qy 193 AlaIleProHisGlySerArgValLysIleArgPheAspThrProSerGlyValLysAsp 212
Db 675 CTAATTCCTCATGATCTCGTGAAGGTGAGATGATCTCCATCGAGGATTAAGAT 734
Qy 213 SerIleSerAlaTyrIleLysPheSerValGlnAlaProGlyGlnIleProPheAsnGly 232
Db 735 TCATTTCCAGCTCGATCAAGTACTCACTGACGCGCCACAGGAATACCATATGATGGG 794
Qy 233 IleTyrTyrAspProProGlnGlnLysTyrValPheGlnHisProGlnProLysArg 252
Db 795 ATTATATATGATCTCTCGAAGAGGTAAAGATATGTGTTCAGCATGCGCACTTAACA 854
Qy 253 ProGlnSerLeuArgGlyIleTyrGlnSerHisIleGlyMetSerSerProGluProLysIle 272
Db 855 CCAAAATCATTCGGATATATGAAACACATGTCGGAATGAGTACCCGGAACCGAAGTA 914
Qy 273 AsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgGlnGlyTyrAsn 292
Db 915 AACACATATGTAATCTTAAAGGATGAAGTCCTCCCAAGATTAATAAACTTGGATCAAT 974
Qy 293 AlaValGlnIleMetAlaIleGlnGlnHisSerTyrTyrAlaSerPheGlyTyrHisVal 312
Db 975 GCACTGCAAAATTAATGCGAATCCAGAGCACTCATATATGAGAAGCTTTGAAATCACTGA 1034
Qy 313 ThrAsnPhePheAlaProSerSerArgPheGlyTyrProGlnAspLeuLysSerLeuIle 332
Db 1035 ACTATATTTTTTGGCCCAAGTAGTGTGTTGGATCCCAAGAGATTTGAAGCTTTGATT 1094
Qy 333 AspArgAlaHisGlyLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer 352
Db 1095 GATAGAGACATGACCTTGTTGCTAGTCTCATGATGTGGTTCATAGTCATGCGCTCA 1154
Qy 353 AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly 372
Db 1155 AGTATATCTCTGGATGGGTGATGTGTTGATGTGACGATACACATTAACATTTCAAGT 1214
Qy 373 GlyProAspGlyHisHisTyrMetTyrAspSerArgLeuPheAsnTyrGlySerTyrGlu 392
Db 1215 GGTCCACGTGGCCATCACTGAGTGTGGATTTCTCGCTATTTACATATGGGAATGGGA 1274
Qy 393 ValLeuArgPheLeuLeuSerAsnAlaArgTyrTyrLeuGlnGlyTyrLysPheAspGly 412
Db 1275 GTTTTAAGTTTCTCTCTCCATGTAGTGTGCTCGAAGAAATATAAGTTGATGTG 1334
Qy 413 PheArgPheAspGlyValThrSerMetMetTyrThrHisHisGlyLeuGlnMetThrPhe 432

Db 1335 TTCGCTTTGATGATGTGACCTTCATGATGATACCTCACACGAGATTACAGTACATTT 1394
Qy 433 ThrGlyAsnTyrGlyGlnTyrPheGlyPheAlaThrAspValAspAlaValTyrLeu 452
Db 1395 ACGGGGAATCTCAAGATGATTTTGGCTTGGCCACGATGTATGATGACAGTGTACTTG 1454
Qy 453 MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGlnAsp 472
Db 1455 AGCTCGGTAAATGATCTAATTCATGATGACCTTATCCGAGGCTGTAAACCATTTGGAAAT 1514
Qy 473 ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr 492
Db 1515 GTTATGTAATGCTTCAATTTGCTTCTCTGTTACAGATGTGGGTAGTGTGACTAT 1574
Qy 493 ArgLeuHisMetAlaValAlaAspLysTyrIleGlnLeuLeuLysGlnSerAspGlySer 512
Db 1575 CGATGCAATATGGCTGTGCTGACCAATGATGATGACCTTCAAGCAAGATGAATACT 1634
Qy 513 TrrPlySerGlyAspIleValHisTyrLeuThrAsnArgTrrPheGlnLysCysVal 532
Db 1635 TGGAAATGGGTGATATTTGTGCACACATGACAATATGGAGGTGTATGAGAAATGTGTA 1694
Qy 533 ThrTyrAlaGlySerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTyrLeu 552
Db 1695 ACTTATGCTGAATCATGATCATGATCAAGCATTAAGTCGGCGACAAAGCATATGGCTTGGT 1754
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/ Patent No. US20020002713A1
/ GENERAL INFORMATION:
/ APPLICANT: Allen, Steve
/ APPLICANT: Beckles, Diane M.
/ APPLICANT: Butler, Karla
/ APPLICANT: Pearlstein, Rich
/ TITLE OF INVENTION: Starch Branching Enzyme IIB
/ FILE REFERENCE: B01439 US NA
/ CURRENT APPLICATION NUMBER: US/09/792.127
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 60/186098
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 1
/ LENGTH: 2559
/ TYPE: DNA
/ ORGANISM: Triticum aestivum
US-09-508-377-12 (1-768) x US-09-792-127-1 (1-2559)

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Score: 3329.00 Matches: 589
Percent Similarity: 94.06% Conservative: 60
Best Local Similarity: 85.36% Mismatches: 41
Query Match: 79.85% Indels: 0
DB: 9 Gaps: 0

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 US-10-424-599-130849
 ; Sequence 130849, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 130849
 ; LENGTH: 5164
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 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_89164C.1
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 Best Local Similarity: 77.85% Mismatches: 75
 Query Match: 79.29% Indels: 22
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 DB 1738 TATCATGATGATGAGATTCCTGCTTTTAACTACGAAAGCTGGAACTTAAAGTAT 1797
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US-09-938-842A-872
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; Patent No. US20020160378A1
; GENERAL INFORMATION:

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us-09-508-377-12.rnpb

Page 12

Db 2218 TACGCATGTGTTGCTCCAGCCTGGAAAAATATAGATCGATTGGATCGGACGATCCT 2277

QY 725 LeuPheGlyGlyPheSerArgLeuAspHisAspValAspIlyrPheThrThrGluHisPro 744

Db 2278 CTCCTTTGTGTGATTCATCAATGGCTCGATCGCAAGGCGAGTCTTCACATTAGAGCGCTTA 2337

QY 745 HisAspAsnArgProArgSerPheSerValIlyrThrProSerArgThrAlaValValTyr 764

Db 2338 TACACGACACGACCGTGTCTCTTCATGCTCATGCACCGGTAGAACCGCGGTGGTTAT 2397

QY 765 AlaLeu 766

Db 2398 GCTTTA 2403

```

RESULT 9
US-10-239-145-1
; Sequence 1, Application US/10239145
; Publication No. US20040068766A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
TITLE OF INVENTION: Enzyme
FILE REFERENCE: P8156.WO
CURRENT APPLICATION NUMBER: US/10/239,145
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: GB 0006733.0
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 2563
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SBHII CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(2549)
US-10-239-145-1

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Alignment Scores:	
pred. No.:	0
Score:	3197.00
Percent Similarity:	82.778
Best Local Similarity:	72.618
Query Match:	76.69%
DB:	12
	6
	Gaps: 6
	length: 2563
	Matches: 586
	Conservatives: 82
	Mismatches: 91
	Indels: 48
	12
	6

US-09-508-377-12 (1-768) x US-10-239-145-1 (1-2563)

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QY      2 AlaThrPheAlaValSerGlyAlaThrLeu-----GlyValAlaArgProPheAlaAla 19
      :::
Db      114 TCtACAGTTGCAGCACTCGGGGAAAGCTTGTGCTCGGAACCCAGAGTATAGCTCTCA 173
      ::::
QY      20 AlaGlnProGluGlnLeuGlnLileProGlu-----
      ::::
Db      174 TCCTCAACAGACCAATTGATTCACCTAGAGACATCTCCAGAAATATCCACAGATCAACT 233
      ::::
QY      30 AspLileGlnGlnGlnThrAlaGlu-----
      ::::
Db      234 GATGTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAACTGAGAACGATGACGTT 293
      ::::
QY      38 -----ValAsnMetThrGlyGlyThrAlaGlu-----
      ::::
Db      294 GAGCGCTCAAGATGATCTTACAGAAAGTGTGAAGACTGATTTGCTTCATCATCAACA 353
      ::::
QY      47 -----LysLeuGlnSerSerGluProThrGlnLylLileValGlnThrIle 61
      ::::
Db      354 CTACAGAAAGCGTGCTAACTCGAGAGAGCTCTAAACAATTAAATCTTTGGAAGAGACATT 413
      ::::
QY      62 ThrAspGlyValThrIlyscGlyValLysGlnLeuValValGlyGluLysProAlaGlyVal 81
      ::::
Db      414 ATTGTAGTAATCTGATAGT---ATCAACAAGG-----AGGGGATC 449
      ::::

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QY	82	ProlyserProGlyIAspGlyGlnIysIleTyrGlnIleAspProThrIleuYAspPheArg	101
Db	450	CCTCCACCTGGACCTGGTCAGAAATATTATGAATTAACCCCTTTTGACAACTATCGT	509
QY	102	SerIleuAspIYrAcGTYrSergIuTYrArgArgIleArgAlaIleAspGlnHis	121
Db	510	CAACACCTTGATTACAGGTATTCACATACAGAACTAGGAGGAGCAATTGACAACTAT	569
QY	122	GluGlyGlyLeuGlnAlaPheSerArgIlyTyrGlnIuSLeuGlyPheThrArgSerAla	141
Db	570	GAGGATGGATTGGAAAGCTTTTTCGTGGTATTAAAAAAATGGGTTTCACCTCGTAGTCCT	629
QY	142	GluGlyIleThrTYrAcGluUTPAlaProGlyValHisSerAlaAlaIleValAlYAsp	161
Db	630	ACAGGTATCACTTACCGTAGATGGAGGACCTCGTGTCGCCAGTCAGCTGCCCTCATTTGAGAT	689
QY	162	PheAsnAsnTPraPsnProAsnAlaAspThrMetThrArgAspIYrGlyValTyrGln	181
Db	690	TTCAACATATGGACAGCGAAATGCTGACATATATGCTCGCATGATGATTTGGTCTGGAG	749
QY	182	IlePheIeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIys	201
Db	750	ATTTTTTCGCCAAATAATGGAGAGGTTCTCTCCGCAATTCCTCATGGGCTCAGAGTAAG	809
QY	202	IleArgMetAspTPrProSergIlyValIleAspSerIleSerAlaTPrIleYAspPheSer	221
Db	810	ATACGTATGACACTCCATCAGAGGTTTAAAGATTCCTCTCGTTGGATCACTACTCT	869
QY	222	ValGlnAlaProGlyGlnIleProPheAsnGlyIleTyrTYrAspProProGluGlnIu	241
Db	870	TTACAGCTTCCTGATGAATTCCTATTAATAGGATATATTATGATCCACCCGGAAGAGAG	929
QY	242	LysTYrValPheGlnHisProGlnProIuYArgProGluSerIleuArgIleTyrGluSer	261
Db	930	AGGATATCTTCCACACCCACGGCCAAAGAAACAAAGTCCGTGAGATATTAATTAATCT	989
QY	262	HisIleGlyMetSerSerProGluProIuYIleAsnSerTYrAlaAsnPheArgAspGlu	281
Db	990	CATTGGAAATGATTAAGTCGCGAAGCTTAAATTATCAATCAATCGAATTTTACAGATGAA	1049
QY	282	ValIeuProArgIleIyAsnArgLeuGlyTYrAsnAlaValGlnIleMetAlaIleGlnIu	301
Db	1050	GTTCTTCCTCCCAAAAAAAGCTTGGGTACATCCGTCGCAAAATTATGGCTATTCACAGG	1109
QY	302	HisSerTYrTYrAlaSerPheGlyTYrHisValThrAsnPhePheAlaProSerSerArg	321
Db	1110	CATTCTATTTATGCTAGTTTGGTTTACATGTCACAAATTTTTTTGACACCAAGACCGCT	1169
QY	322	PheGlyThrProGluAspLeuIleYSerIleuIleAspArgAlaHisGlyLeuGlyLeuIeu	341
Db	1170	TTTGGAACTCCCGACGACCTTAACTCTTTGATTATAAAGCTCATGAGCTTGAGATTTGTT	1229
QY	342	ValIeuMetAspIleValHisSerHisSerSerAsnAsnThrIleuAspGlyIleuAsnGly	361
Db	1230	GTTCTCATGACATTTGTCACAGCAATGACCAAAATATATCTTTAGATGACTAAACATG	1289
QY	362	PheAspGlyThrAspThrHisIstYrPheHisGlyIleProArgGlyHisIstYrMetIleTP	381
Db	1280	TTTACAGGCAACAGATAGTTGTTACTTTCACTCTGAGAGCTGTGGTTATCATTTGATGGG	1349
QY	382	AspSerArgLeuPheAsnTYrGlySerTyrGluValIleuArgPheIleuIleSerAsnAla	401
Db	1350	GATTCGCCGCTTTTAACTATGAGAACTGGAGGTACTAGATATCTTCTCTCAAAATGCG	1409
QY	402	ArgTPrTPrIleuGlnIuTYrIlePheAspIyPheArgPheAspGlyValIThrSerMet	421
Db	1410	AGATCGTGCTGATGATGACTTCAATTTTGAATGGATTTTGAATTTGATGGTGATCAATCAATG	1469
QY	422	MetTYrThrHisHisGlyLeuGlnMetThrPheThrArgIYAsnTYrGlyGluTYrPheGly	441
Db	1470	ATGTGTACTCCACGAGATTAATCCGTGGAGATTCACTGGGAACTACGAGGAATATCTTTGGA	1529


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QY 442 PheAlThrAspValAspAlaValValTyrLeuMetLeuValAsnProLeuIleHisGly 461
DB 1530 CTGGCAACTGATGATGCTGTTGATGATGATGCTGCTCAACGATCTTATTCATGAGG 1589
QY 462 LeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIle 481
DB 1590 CTTTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1649
QY 482 ProValProAspGlyValValGlyPheAspTyrArgLeuHisMetAlaValAlaAspLys 501
DB 1650 CCCGTTCAAGATGGGGGCTGTTGCTTGGATGATGCTGCTGATGCGCATATGGCATATGGCATATAA 1709
QY 502 TrpIleGluLeuLeuLysGlnSerAspGluSerTrpLysMetGlyAspIleValHisThr 521
DB 1710 TGGATTGAGTTGCTCAAGAAACGGAGATGAGATGAGATGAGATGAGATGATGATGATGATCA 1769
QY 522 LeuThrAsnArgArgTrpLeuGluLysCysValThrTyrAlaGluSerHisAspGlnAla 541
DB 1770 CTGACAAATGAGATGCTGGAAAGTGTGTTCAATGCTGGAAGTCATGATCAAGTCACT 1829
QY 542 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 561
DB 1830 CTAGTGGTGATATAAATAATAGATTTGCTGCTGATGCGCAAGATATGATGATTTTATG 1889
QY 562 AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMetIle 581
DB 1890 GCTCTGATGAGCCGTCACATCATTAATGATGCTGGAATGAGCATTCACAGATGATGAT 1949
QY 582 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnProMetGlyAsnGluPhe 601
DB 1950 AGCGTTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2009
QY 602 GlyHisProGluTrpIleAspPheProArgGlyProGlnThrLeuProThrGlyLysVal 621
DB 2010 GGGCACCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2069
QY 622 LeuProGlyAsnAsnAsnSerTyrAspLysCysArgAlaGlyPheAspLeuGlyAspAla 641
DB 2070 ATTCGCCGAAACCAATTCAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2129
QY 642 AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLysGluGlu 661
DB 2130 GATTTATTTAGATACCGTGGTGTGCAAGATTTGACCGGCTATGCAATGATTTTGAAGAT 2189
QY 662 LysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGlnGluAspLys 681
DB 2190 AATATATAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2249
QY 682 ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTrpSerAsnSer 701
DB 2250 ATGATTTATTTGAAAAAGAAACCTAGTTTGTCTTAAATTTTCACTGCGCAAAAAAGC 2309
QY 702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAspSer 721
DB 2310 TATTCACACTATGCAATGAGCTGCTGAGGCTGGAATAATACAGAGTTGCTTGGACTGCTG 2369
QY 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741
DB 2370 GATGATCACTTTTGGTGGCTTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2429
QY 742 GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761
DB 2430 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2489
QY 762 ValValTyrAlaLeuThrGlu 786
DB 2490 GTGGTTATGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2510
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RESULT 10
US-10-056-454A-17
; Sequence 17, Application US/10056454A
; Publication No. US20030166919A1
; GENERAL INFORMATION:
```

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APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unidema Blvd.
CITY: Newcasttle
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-10-056-454A-17
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-056-454A-17
Alignment Scores:
Pred. No.: 0 Length: 2529
Score: 3196.00 Matches: 586
Percent Similarity: 82.53% Conservative: 80
Best Local Similarity: 72.61% Mismatches: 93
Query Match: 76.66% Indels: 48
DB: 14 Gaps: 6
US-09-508-377-12 (1-768) x US-10-056-454A-17 (1-2529)
QY 2 AlaThrPheAlaValSerGlyAlaThrLeu-----GlyValAlaArgProProAlaAla 19
DB 92 TCAACAGTTGACGATCGGGGAAAGTCTTGCTGCGTGAAYCCAGATGATGCTCTCA 151
QY 20 AlaGlnProGlnGluLeuGlnIleProGlu----- 29
DB 152 TCCTCAACAGACCAAATTGATGATCTAGATGACATCTCCAGAAATTCGCCAGATCAACT 211
QY 30 AspIleGluGlnThrAlaGlu----- 37
DB 212 GATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 271
QY 38 -----ValAsnMetThrGlyGlyThrAlaGlu----- 46
DB 272 GAGCCGTCAGAGATCTTACAGAGAGTGTGAAGAGCTGATTTTCTTCATCACTACAA 331
QY 47 -----LysLeuGluSerSerGluProThrGlnGlyIleValGluThrIle 61
DB 332 CTACAAAGAGTGTAACTGAGAGAGTCTAAACATTAATCTTGAAGAGCATTT 391
QY 62 ThrAspGlyValThrIleGlyValLysGluLeuValValGlyGluLysProArgValVal 81
DB 392 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 427
QY 82 ProLysProGlyAspGlyGluLysIleTyrGluIleAspProThrLeuLysAspPheArg 101
DB 428 CCTCCACCTTGACTGCTGAGAGATTTATGAATATGACCCCTTTGACAAACTATGCT 487
QY 102 SerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAlaAlaIleAspGlnHis 121
DB 488 CAACACCTTGATTTACGGTATTCACAGTACAGAAATCGAGGAGGCAATGACAGAT 547
QY 122 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGlyLysLeuGlyPheThrArgSerAla 141
DB 548 GAGGAGGTTTGGAACTTTTCTCGGTGTTATGAAAAAATGGGTTTCACCTGATGCT 607
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QY 142 GluGlyIleThrTYRArgGluTrpAlaProGlyAlaHisSerAlaAlaLeuValGlyAsp 161
 Db 608 ACAGGTATCACTTACCGTGAAGGCTCTCTGGTGCAGATGAGCTGCCCTCATTTGAGAT 667
 QY 162 PheAsnAntPAsnProAsnAlaAspThrMetThrArgAspAspTYRGLYValTrpGlu 181
 Db 668 TTCAACAATTGGGACGCAAAATGCTGACATTATGACTCGGAATGAATTTGGTCTGGGGAG 727
 QY 182 IlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgVallys 201
 Db 728 ATTTTTCGCAAAATATGTGATGTCTCTCGCAATTCCTCAATGGGTCCGAGATGAAG 787
 QY 202 IleArgMetAspThrProSerGlyValIysAspSerIleSerAlaTrpIleLysPheSer 221
 Db 788 ATACGATGACACCTCCATCAGGTGTAAAGATTCATTCCTGCTGGATCAACTACTCT 847
 QY 222 ValGlnAlaProGlyGluIleProPheAsnGlyIleTYRTrpAspProProGlyGlu 241
 Db 848 TTACAGCTTCTCTGATGAATTCATATATGAAATATATATGATCCACCAGAGAGAG 907
 QY 242 LysTYRValPheGlnHisProGlnProLysArgProGlyLysLeuArgTleTYRTrpGlySer 261
 Db 908 AGGTATATCTTCACACCCAGCCGCAAGAAACCAAGTCCCTGAGATATATGATAT 967
 QY 262 HisIleGlyMetSerSerProGlyLysIleAsnSerTYRAlaAsnPheArgAspGlu 281
 Db 968 CATATGGAAATGAGTATGCTCCGAGCTAAATTAATTAATCACTACGTGATTTAGAGATGA 1027
 QY 282 ValLeuProArgGlyIleLysArgLeuGlyTYRAsnAlaValGlnIleMetAlaIleGlnGlu 301
 Db 1028 GTTCTTCTCCCATAAATAASCTTGGGTACATGCGGTGCAATATATGCTATTCAGAG 1087
 QY 302 HisSerTYRTrpAlaSerPheGlyTYRHisValThrAsnPhePheAlaProSerSerArg 321
 Db 1088 CATCTTATTTATGCTAGTTTGGTATCATGTCACAAAATTTTTCACACAGACCCCT 1147
 QY 322 PheGlyThrProGlyAspLeuLysSerLeuIleAspArgAlaHisGlyLeuGlyLeu 341
 Db 1148 TTGGAAACGCCGACGACCTTAAGCTTTGATTGATTAAGCTCATAGCTAGGAATTTGTT 1207
 QY 342 ValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGly 361
 Db 1208 GTTCCATGAGCATGTTCTCACAGCATGATCAAAATATATCTTAATGAGCTGAGACATG 1267
 QY 362 PheAspGlyThrAspThrHisTYRHisGlyGlyProArgGlyHisHisTrpMetTrp 381
 Db 1268 TTGACGGACAGATAGTTGTTACTTCTCTGAGAGCTCGTGGTATATCATTTGAGTGTG 1327
 QY 382 AspSerArgLeuPheAsnTYRGLYSerTrpGlyValLeuArgPheLeuLeuSerAsnAla 401
 Db 1328 GATTCGCCCTCTTTAATCATATGAAACCTGGAGAGTCTTAGGATCTTCTCTCAAAATGCG 1387
 QY 402 ArgTrpTrpLeuGlyGlyTYRTrpPheAspGlyPheArgPheAspGlyValThrSerMet 421
 Db 1388 AGATGGTGGTGGATGAGTTCAAAATTTGATGATTTAGATTGATGATGAGATCATCATG 1447
 QY 422 MetTYRThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTYRGLYGlyIleTYRTrpGly 441
 Db 1448 ATGTATATCTCACACAGGATTAATCGGTGGATTCACCTGGAACTACAGAAATCTTTGCA 1507
 QY 442 PheAlaThrAspValAspAlaValValTYRLeuMetLeuValAsnAspLeuIleHisGly 461
 Db 1508 CTCGACATGATGATGCTGTGTGTATCTGATCTGCTGATCAACATCTTATTCACGGG 1567
 QY 462 LeuHisProAsnAlaValSerIleGlyGlyAspValSerGlyMetProThrPheCysIle 481
 Db 1568 CTTTTCGAGATGCAATTCATTTGATGAGATGTTAGCGGAATGCGGACATTTTGTATT 1627
 QY 482 ProValProAspGlyValGlyPheAspTYRArgLeuHisMetAlaValAlaAspLys 501
 Db 1628 CCCGTTCAAGATGGGGCTGTGGCTTTGACTATCGGCTGATATGGAATTTGCTGATTA 1687
 QY 502 TrpIleGlyLeuLeuLysGlnSerAspGlySerTrpLysMetGlyAspIleValHisThr 521

Db 1688 TGGATTGAGTTGCTCAAGAAACGGGATGAGGATTTGAGAGTGGTGTATTTGTTCAATCA 1747
 QY 522 LeuThrAsnArgArgTrpLeuGlyLysCysValThrTYRAlaGlySerHisAspGlnAla 541
 Db 1748 CTCACAAATTAAGAAATGCTGGGAAATGCTGTTTCAATCCCTGAAATGATCAATCAAGCT 1807
 QY 542 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTYRAspPheMet 561
 Db 1808 CTAGTCGATGATAAACTATATAGCATTCGCTGATGAGCAAGGATATGATGATTTATG 1867
 QY 562 AlaLeuAspArgProSerTrpProArgIleAspArgGlyIleAlaLeuHisLysMetIle 581
 Db 1868 GCTCTGATATGACCGCAACAYCATTAATATATGATGATGGATGATTCGACAAAGTATT 1927
 QY 582 ArgLeuValThrMetGlyLeuGlyGlyTYRLeuAsnPheMetGlyAsnGlyPhe 601
 Db 1928 AGCTTGTATCTATGGAATATAGAGAGAAAGGTACTAATTTCAATGGAAATGATTC 1987
 QY 602 GlyHisProGlyLysTrpIleAspPheProArgGlyProGlnThrLeuProThrGlyLysVal 621
 Db 1988 GGCACCCCTGAGTGAATTTGATTTCCCTAGGGCTGARGACACCTCTGTGATGCTCACTA 2047
 QY 622 LeuProGlyAsnAsnAsnSerTYRAspLysCysArgArgArgPheAspLeuGlyAspAla 641
 Db 2048 ATTCGCGGAAACCAATTCAGTTATGATTAATGACACGAGATTTGACCTGGAGATGCA 2107
 QY 642 AspPheLeuArgTYRHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGlnGlu 661
 Db 2108 GAATATTATTAAGATACATGAGTGTTCAGAAATTTGACCGGGTATGACATATCTTAAGAT 2167
 QY 662 LysTYRGLYPheMetTrpSerGlyHisGlnTYRValSerArgGlyHisGlyGlyLysAsp 681
 Db 2168 AAATATGAGTTTATGACTTACAGAACACAGTCTCATCAACAAAGATGAAGAGATAGG 2227
 QY 682 ValIleIlePheGlnArgGlyAspLeuValPheValPheAsnPheHisTrpSerAsnSer 701
 Db 2228 ATGATGTATTTGAAGAAGAAACCTGATTTGTCTTAAATTTTCACTGACGCAAAATAC 2287
 QY 702 PhePheAspTYRArgValGlyCysSerArgProGlyLysTYRValValAlaLeuAspSer 721
 Db 2288 TATTCAGACTATGCCAATAGCTGCTGAGCTTGAAATATCAAGTTGGCTTGACTCA 2347
 QY 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTYRTrpThr 741
 Db 2348 GATGATCACTTTTGGTGGCTTGGGAGATTAATGATATATGCGCAATATTTCACTCT 2407
 QY 742 GlnHisProHisAspAsnArgProArgSerPheSerValTYRThrProSerArgThrAla 761
 Db 2408 GAAGGATCGATGATGATGCTCCCTGTCAATTTGATGATGATGACCTTAGTGAACAGCA 2467
 QY 762 ValValTYRAlaLeuThrGlu 788
 Db 2468 GTGCTCATGCACTATGATGAC 2488

RESULT 11
 US-10-056-454A-19
 Sequence 19, Application US/1005645A
 Publication No. US20030166919A1
 GENERAL INFORMATION:
 APPLICANT: National Starch and Chemical Investment Holding Corporation
 TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: National Starch and Chemical Investment Holding Corporation
 STREET: 1000 Unigema Blvd.
 CITY: Newcastle
 STATE: Delaware
 COUNTRY: United States of America
 ZIP: 19720
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS					
SOFTWARE: Patentin Release #1.0, Version #1.30					
CURRENT APPLICATION DATA:					
APPLICATION NUMBER: US/10/056,454A					
FILING DATE: 25-Jun-2002					
INFORMATION FOR SEQ ID NO: 19:					
SEQUENCE CHARACTERISTICS:					
LENGTH: 2578 base pairs					
TYPE: nucleic acid					
STRANDEDNESS: single					
TOPOLOGY: linear					
SEQUENCE DESCRIPTION: SEQ ID NO: 19:					
US-10-056-454A-19					
Alignment Scores:					
Pred. No.:	0	Length:	2578		
Score:	3189.00	Matches:	585		
Percent Similarity:	82.40%	Conservative:	80		
Best Local Similarity:	72.49%	Mismatches:	94		
Query Match:	76.49%	Indels:	48		
DB:	14	Gaps:	6		
US-09-508-377-12 (1-768) x US-10-056-454A-19 (1-2578)					
QY	2	AlaThrPheAlaValSerGlyAlaThrLeu-----GlyValAlaArgProProAlaAla	19		
DB	99	TCTAAGTTGACGACATCGGGAAAGTCCTTGCTGCGAACCAGAGTGATGACTCTCA	158		
QY	20	AlaGlnProGluGluLeuGlnIleProGlu-----	29		
DB	159	TCCTCAACAAACCAATTGATTCACCTGACACATCCGAGAAATGCCAGATCACT	218		
QY	30	AspIleGluGluThrAlaGlu-----	37		
DB	219	GATGTAGATGATTCAACATGGAAACAGCTAGCCAGATTAAACTGAGAACGATGACGT	278		
QY	38	-----ValAsnMetThrGlyGlyThrAlaGlu-----	46		
DB	279	GAGCGGTCAAGTATCTTACAGAGAGTGTGAAAGACTGGATTGCTTCATCACTACAA	338		
QY	47	-----LysLeuGlnSerSerGluProThrGlnGlyIleValAlaGluThrIle	61		
DB	339	CTACAAAGAGGTGATTAAGTGAAGAGCTTAAACATTAAATCTCTGAAGACAT	398		
QY	62	ThrAspGlyValThrIleGlyValIleValIleValIleValIleValIleValIleValIle	81		
DB	399	ATTGATGATCTGATGAG--ATCAGAGAG-----AGGGGCGATC	434		
QY	82	ProLysProGlyAspGlyGlnIleValIleValIleValIleValIleValIleValIleValIle	101		
DB	435	CCTCACTGCGCTTGTGCAAGAGATTGAAATGAGCCCTTTTGACAAACTATGCT	494		
QY	102	SerHisLeuAspThrArgIleSerGluThrArgArgIleArgAlaAlaIleAspGlnHis	121		
DB	495	CAACACCTTGATTACAGGATTCACAGTACAGAACTGAGGAGGCAATTGACAAATAT	554		
QY	122	GluGlyGlyLeuGluAlaPheSerArgIleValIleValIleValIleValIleValIleValIle	141		
DB	555	GAGGGGTGTTTGAAGCTTTTCTCGTGTATGAAATAATGGGTTTCACTCGTAGTCT	614		
QY	142	GluGlyIleThrThrArgGluThrArgIleValIleValIleValIleValIleValIleValIle	161		
DB	615	ACAGGATACCTTACGAGTGGGCTCTGCTGCGCCAGCTCAAGTCCCTCATTTGGAGAT	674		
QY	162	PheAsnAspThrAsnProAsnAlaAspThrMetThrArgAspArgIleValIleValIleValIle	181		
DB	675	TTCACAAATTTGGGACCCAAATGCTGACATATGACTCGAATGAAATTTGGTGTGGAG	734		
QY	182	IlePheLeuProAsnAlaAspGlySerProAlaIleProHisGlySerArgValIle	201		
DB	735	ATTTTCTCCCAATATGATGATGATGTTCTCCGCAATTCCTCATGGGTCCAGAGTAAAG	794		
QY	202	IleAsnMetThrProSerGlyValIleValAspSerIleSerAlaThrIleValIleValIleValIle	221		

DB	795	ATACGTATGACATCTCCATGAGTGTTAAGATTCATTCCTCGCTTGGATCAACATCTCT	854		
QY	222	ValGlnAlaProGlyGluIleProPheAsnGlyIleValIleValIleValIleValIleValIle	241		
DB	855	TCACAGCTTCTGTATGAAATTCATATATGAAATATATATATATATATATATATATATAT	914		
QY	242	LysIleValPheGlnHisLeuProGlnProLysArgProGlnSerLeuArgIleValIleValIle	261		
DB	915	AGGTATATCTTCCAAACCCAGCGCCAAAGAAACCAAGTCCCTGAGATATATATATCT	974		
QY	262	HisIleGlyMetSerSerProGluProLysIleAsnSerValAsnPheArgAspGlu	281		
DB	975	CATATTGGAATGAGTAGTACGCCAGCCTAATAATTACTCATACGTGATTTTAGAGATGAA	1034		
QY	282	ValLeuProArgIleValArgLeuGlyThrAsnAlaValGlnIleMetAlaIleGlnGlu	301		
DB	1035	GTTCTTCTCCGCAATAAAGCTTGGTACATGCGGTGCAATGATATATGACTTTCAGAG	1094		
QY	302	HisSerIleValAspPheGlyThrHisValThrAsnPheAlaProSerSerArg	321		
DB	1095	CATCTTATATGCTAGTGTGTTATCATGTCACAAATTTTGTGACCAAGCACCCGT	1154		
QY	322	PheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHisGlyLeuGlyLeuLeu	341		
DB	1155	TTTGAAGCCCGACGACGACCTTAAGCTTGTGATTGATTAAGCTCAGAGCTAGGAATGTT	1214		
QY	342	ValLeuMetAspIleValHisSerHisSerAsnAsnThrLeuAspGlyLeuAsnGly	361		
DB	1215	GTTCTCATGACATGTTCAAGCCATCATCAATTAATCTTGTAGATGACGTGAACATG	1274		
QY	362	PheAspGlyThrAspThrHisIleThrPheHisGlyGlyProArgGlyHisIleStrMetTrp	381		
DB	1275	TTTGAAGCCCGACGACGACGTTTACTTCACTCTGAGCTCGGTATATATGGAATGG	1334		
QY	382	AspSerArgLeuPheAsnIleGlySerTrpGluValLeuArgPheLeuSerAsnAla	401		
DB	1335	GATTCGCCCTTTTAACTATGAGAAACCTGGAGGTACTAGTATCTTCTCCAAATGCG	1394		
QY	402	ArgTrpIleLeuGluGlyThrLysPheAspGlyPheArgPheAspGlyValThrSerMet	421		
DB	1395	AGATGCGGTGTTGATGAGTGAATTAATGATGATGATGATGATGATGATGATGATGATG	1454		
QY	422	MetTrpThrHisHisGlyLeuGlnMetThrPheThrGlyAsnIleGlyIleValIleValIle	441		
DB	1455	ATGATATCTCACACGAGTATTCGGGTGATTCATCTGGAACTTACAGAAATCTTTGGA	1514		
QY	442	PheAlaThrAspValAspAlaValValIleValIleValIleValIleValIleValIleValIle	461		
DB	1515	CTCGCAATGATGAGTGCCTGTTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG	1574		
QY	462	LeuHisProAspAlaValSerIleGlyLeuAspValSerGlyMetProThrPheGlyIle	481		
DB	1575	CTTTTCCCAATGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1634		
QY	482	ProValProAspGlyValValGlyPheAspThrArgLeuHisMetAlaValAlaAspLys	501		
DB	1635	CCCGTTCAAGATGGGGGCTTGGCTTTGATCTTACCTGCTGATGATGATGATGATGATG	1694		
QY	502	TrpIleGluLeuLeuLysGlnSerAspGlnSerTrpLysMetGlyAspIleValHisTrp	521		
DB	1695	TGATGTGCTGCTCAAGAAACGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG	1754		
QY	522	LeuThrAsnArgArgTrpLeuGlyLysCysValIleThrValGlnSerHisAspGlnAla	541		
DB	1755	CTGCAAAATTAAGATGTGCGAAAGATGTTTATATAGCTGAAAGTATGATGATGATG	1814		
QY	542	LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTrpAspPheMet	561		
DB	1815	CTAGTGGTGAATTAACATATGATGATGATGATGATGATGATGATGATGATGATGATG	1874		
QY	562	AlaLeuAspArgProSerThrProArgIleAspArgIleAlaAlaLeuHisLysMetIle	581		

Db 1875 GCCTCGATGATGACCCGCAACATCATTAATGATGCTGGGATAGCATTTGCACCAATGATTT 193

QY 582 ATGLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnProMetGlyAsnGluPhe 601

Db 1935 AGCGTTTAACTATGATGGATTAGGAGGGAGAAAGGGTAACTTAATTTTCATGCGAAAGAATTC 1994

QY 602 GlnHisProGluTyrPileAspPheProArgGlyProGlnThrLeuProThrGlyLeuVal 621

Db 1995 GGGCACCCCTGAGTGGATGATTGATTTCCCTTAAGGGCTGAACAACCTCTCTGATGACTCAGTA 2054

QY 622 LeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 641

Db 2055 ATTCGCCGAAACCAATTCAGTTATGATGAATAAGCAGACGAGATTTGACCTGGGAGATGCA 2114

QY 642 AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661

Db 2115 GAATATTAAAGATACCGTGGGTTGCCAAGAAATTTACCGGGCTATGACGATATCTTGAAGAT 2174

QY 662 LysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGluGluAspLys 681

Db 2175 AATATATAGTTTATGACTTCAGAACACCACTCATATCCAGAAAGATGAAGAGATAG 2234

QY 682 ValIleIlePheGluArgGlyAspLeuValPheValPheAsnProHisTyrSerAsnSer 701

Db 2235 ATGATGTATTTGAAAAAGGAACCTGATTTTGTCTTAAATTTTCATCGACAAAAAGC 2294

QY 702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLeuValAlaLeuAspSer 721

Db 2295 TATTCACACTATCCCATAGGCTGCTCGTAGAGCTGGAAAAATCAAGATTGCTTGACCTCA 2354

QY 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741

Db 2355 GATCATCCACTTTTGGTGGCTTGGGAGATTAATGATTAAGCGCAATATTCGACCTTT 2414

QY 742 GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761

Db 2415 GAAGAGATGTATGTATGATCGTCTCGTTCAATTAATGATGTATGACCTTGTAGAACAGCA 2474

QY 762 ValValTyrAlaLeuThrGlu 768

Db 2475 GTGCTCTATGCACTGATGAC 2495

RESULT 12

US-10-254-1

Sequence 1, Application US/10254534

Publication No. US20030046730A1

GENERAL INFORMATION:

APPLICANT: EK, Bo

APPLICANT: KHOSNODI, Jamshid

APPLICANT: LARSSON, Clas-Tomas

APPLICANT: LARSSON, Hakan

APPLICANT: RASK, Lars

TITLE OR INVENTION: STARCH BRANCHING ENZYME II OF POTATO

FILE REFERENCE: 003300-486

CURRENT APPLICATION NUMBER: US/10/254,534

PRIOR FILING DATE: 2002-09-26

PRIOR FILING DATE: 1998-05-29

PRIOR APPLICATION NUMBER: PCT/SE96/01558

PRIOR FILING DATE: 1996-11-28

PRIOR APPLICATION NUMBER: SE 9504272-7

PRIOR FILING DATE: 1995-11-29

PRIOR APPLICATION NUMBER: SE 9601506-0

PRIOR FILING DATE: 1996-04-19

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 3074

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Belli gene from Solanum tuberosum

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FEATURE:
OTHER INFORMATION: (potato)
/
/
NAME/KEY: CDS
LOCATION: (189)..(2825)
/
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (189)..(332)
/
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
/
FEATURE:
NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
OTHER INFORMATION: n wherein n = A, C, G or T.
/
FEATURE:
NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
OTHER INFORMATION: or Phe.
/
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
/
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
/
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
/
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
/
US-10-254-534-1

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 189.00 Matches: 585
Percent Similarity: 82.78% Conservative: 83
Best Local Similarity: 72.49% Mismatches: 91
Query Match: 76.49% Indels: 48
DB: 14 Gaps: 6

US-09-508-377-12 (1-768) x US-10-254-534-1 (1-3074)

QY 2 AlathrPheAlaValSerGlyAlathrIleu-----GlyValAlAlarProProAlaIa 19
Db ::::|||||
366 TCtCAAGTGGAGCAATCGGGAAAGTCTTGCTGCTGGAACCAAGATGATAGCTCTCA 425
QY 20 AlaginProgluGluLeuGlnIleProglu----- 29
Db ::::|||||
426 TCtCAAGACCAATTTGAGTCACTGAGATCTCCAGAAATTCGCCAGATCAACT 485
QY 30 AspilegluGluInThrAlaGlu----- 37
Db ::::|||||
486 GATGAGATGATGTTCAACAATGAGAACCGCTAGCAGATTAAACTGAGAACGATGCGTT 545
QY 38 -----ValAsnMetThrGlyGlyThrAlaGlu----- 46
Db ::::|||||
546 GAGCGCTCAAGTGAATCTTACAGAAAGTGTGAAGAGCTGAGATTTCCTTCATCATCAAA 605
QY 47 -----LysLeuGluSerSerGluProThrGlnGlyIleValGluThrIle 61
Db ::::|||||
606 CTACAGAAGCGTGTAACCTGAGAGAGCTTAACAACCTTAATATCTCTGAAGAGACAATT 665
QY 62 ThrAspGlyValThrLysGlyValLysGluLeuValValGlyGlyLysProArgValVal 81
Db ::::|||||
666 ATTGATGATCTGATAGG---ATCAAGAGAG-----AGGAGCATC 701

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QY 82 ProlyserProGlyAspGlyGlnIleYrGluIleAspProThrIleuIleAspPheArg 101
Db CCTCACACCTGGAGCTTGGTCAGAGATTATGAAATGACCCCTTTGGACAAATCATACGT 761
QY 102 SerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAlaIleAspGlnHis 121
Db CAACACCTTGAATTACAGTATTCACAGTACAGAACTGAGGAGGCAATTGACAAAGTAT 821
QY 122 GluGlyGlyLeuGlnAlaPheSerArgIleYrGluIleuIleuIlePheThrArgSerAla 141
Db GAGGGTGGTTGGAGCTTTTCTCGTGGTTATGAAAAATAGGTTTCACTCGAGTACGT 881
QY 142 GluGlyIleThrTyrArgGluIleTyrAlaProGlyAlaHisSerAlaAlaLeuValGlyAsp 161
Db ACAGGTATCATCTTACCGTAGTGGGCTCGTGGCCAGTCCAGTCCCTCATTTGAGAT 941
QY 162 PheAsnAsnTyrAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTyrGlu 181
Db TTCAACAATTTGGGACCCAAATGCTGACATTTATGACTCGGAATGAAATTTGGTGTGGAG 1001
QY 182 IlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIys 201
Db ATTTTTCGCCAAATATATGATGGATGGTCTCTGCAATTCCTCATGGGTCCAGAGTGAAG 1061
QY 202 IleArgMetAspThrProSerGlyValIleAspSerIleSerAlaTyrIleIlePheSer 221
Db ATACGTATGGACATCCATCAGTGTGAAGATTCCATTCCTGCTGGATCAACTCTCT 1121
QY 222 ValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGlnGlu 241
Db TTACAGCTTCTCGATGAAATTCATATTAATGAAATATATATATATATATATATATATAT 1181
QY 242 LysTyrValPheGlnHisProGlnProLysArgProGlnSerLeuArgIleTyrGlnSer 261
Db AGGTATATCTTCCAAACACCCAGCCGCAAGAAACCAAGTCCGTGAGAAATATATGATCT 1241
QY 262 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGlu 281
Db CATATTTGAGATAGATGCTCGGAGCCTTAAATTAATCTCATACGTGAATTTTAAAGATGA 1301
QY 282 ValLeuProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGlu 301
Db GTTCTTCTCGCATATAAAAGCTTGGGTACATGCGGTGCAAAATTTATGCTTATTCAGAG 1361
QY 302 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArg 321
Db CATCTTATTAATGATGATTTGGTTATCATGTCACAAATTTTTCGACCAACAGCCGT 1421
QY 322 PheGlyTyrProGluAspLeuLysSerIleuIleAspArgAlaHisGluLeuGlyLeuLeu 341
Db TTTTGAACCCCGACGACCTTAAAGTCTTGAATGATTAAGCTCATAGCTTGAAGATTTGT 1481
QY 342 ValLeuMetAspIleValHisSerHisSerSerSerAsnThrLeuAspGlyLeuAsnGly 361
Db GTTTCATAGCATTTGTTTACAGCCATGCATCAAAATATATCTTATGATGACGAAACATG 1541
QY 362 PheAspGlyTyrAspThrHisTyrPheHisGlyIleProArgGlyHisHisTyrMetTyr 381
Db TTTGACGCGACAGATAGTGTACTTTCACCTCGAGCTCGTGTATATCATTTGAGATGTGG 1601
QY 382 AspSerArgLeuPheAsnTyrGlySerTyrGluValLeuArgPheLeuLeuSerAsnAla 401
Db GATTCGCCGCTCTTAAATATGAAATCGGAGTCTTAAGTATCTTCTCTAAATGCG 1661
QY 402 ArgTyrProLeuGluGluTyrIlePheAspGlyPheArgPheAspGlyValThrSerMet 421
Db AGATGGTGGTTGATGATGATTCAAATTTGATGATTTATGATGATGATGATGATGATGATG 1721
QY 422 MetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyTyrPheGly 441
Db ATGTATACTCACACGAGATTTATCGGTGATTCATCTGCGGAACTACAGAGAAATCTTTGA 1781

Db 1782 CTCGCACTGATGTGAGTGGTGTGTATCTGAATGCTGGTCAACATCTTATTCATGGG 1841
QY 462 LeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIle 481
Db CTTTCCAGATGCAATTAACATTTGCTGAAGTGTATGCGGAATGCGCAATTTTATAT 1901
QY 482 ProValProAspGlyIleValGlyPheAspTyrArgLeuHisMetAlaValAlaAspLys 501
Db CCCGTTCAAGATGGGGGTGTGGCTTTGATGATCTGCGCTCATATGCGCAATTTGTATATA 1961
QY 502 ThrIleGluLeuLeuGlnSerAspGlySerTyrPheMetGlyAspIleValHisThr 521
Db TGGATGTGTTGCTCAAGAAACGGGATGAGATTTGAGAGTGGGTGATATTTGTTCTACA 2021
QY 522 LeuThrAsnArgArgTyrProLeuGluLysCysValThrTyrAlaGlySerHisAspGlnAla 541
Db CTGACAAATAGAAAGATGCTCGGAAAGTGTGTTTATACGCTGAAAGTCATGATCAAGCT 2081
QY 542 LeuValGlyAspLysThrIleAlaPheTyrPheMetAspLysAspMetTyrAspPheMet 561
Db CTAGTCGGTGTAAACATATAGCATTTCTGCTGATGAGAGAAAGAAATATGTATGATTTATG 2141
QY 562 AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisIleMetIle 581
Db GCTGTGATAGACCTTCAACATCATTAATAGATCGTGGATAGCATTCACAAAGATGAT 2201
QY 582 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 601
Db AGGCTTGAATTAATAGGATTTAGAGAGAAAGGATCTTAAATTTGATGGAAATGAAATTC 2261
QY 602 GlyHisProGluTyrIleAspPheProArgGlyProGlnThrLeuProThrGlyIleVal 621
Db GGCCACCTGTAGTATGATTTCCCTAGGGCTGAAACAACCTCTGTATGATGCTCAGAT 2321
QY 622 LeuProGluAsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 641
Db ATTCGCGGAAACCAATTCAGTATGATATGATGACAGAGAAATTTGACCTTGGAGATGCA 2381
QY 642 AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
Db GAATATTTAATATACCGTGGTTCGACAAATTTGACCGGCTATGAGATCTTGAAGAT 2441
QY 662 LysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLeuHisGluGluAspLys 681
Db AAATATAGTATTATGACTTCGAAACACAGATTCATATACGAAAGAGATAGAGATAG 2501
QY 682 ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTyrSerAsnSer 701
Db ATGATGTGATTTGAAAGAAAGCACTAGATTTTGTCTTAAATTTTTCATCTGCAACAAAGC 2561
QY 702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrIleValAlaLeuAspSer 721
Db TATTCAGACTATCCATATGAGCTGCTGAAAGCTGGAATAATACAAAGTCTCTTGGACTCA 2621
QY 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741
Db GATGATCACATTTTGGTGGCTTCGGGGAATGATGATCAATTAAGCCGAAATATTTCACTTT 2681
QY 742 GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761
Db GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2741
QY 762 ValValTyrAlaLeuThrGlu 768
Db GTGGTATATGACATAGTAGAC 2762

RESULT 13
US-10-056-454A-16
Sequence 16, Application US/10056454A
Publication No. US20030166919A1
GENERAL INFORMATION.

TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unidema Blvd.
CITY: Newcasle
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-056-454A-16

Alignment Scores:
Pred. No.: 0 Length: 2576
Score: 3164.50 Matches: 584
Percent Similarity: 82.40% Conservative: 81
Best Local Similarity: 72.37% Mismatch: 94
Query Match: 75.91% Indels: 49
Gaps: 6

US-09-508-377-12 (1-768) x US-10-056-454A-16 (1-2576)
QY 2 AlathrhealvalaIseryIAlathrLeu-----GIYValAlaArgProProAlaala 19
DB 99 TCTACAGTTCAGATCGGGGAAAGTCTTGCTCGGAAACCCAGAGTATGATCTCTCA 158
QY 20 AlagInProglugluLeuGlnleProglu----- 29
DB 159 TCCCAACAAACCAATTGAGTTCAGATCTCCAGAAATTCCCGACATCACT 218
QY 30 AsplleglugluGlnThrAlaglu----- 37
DB 219 GATGTAGTATGTTCAACAATGAGAACACGCTAGCCAGATTAAACTGAGAACATGACGTT 278
QY 38 -----ValAsnMetThrlelyGlyThrAlaglu----- 46
DB 279 GAGCGGTCAAGATCTTACAGAAAGTGTGAAGAGCTGATTTGCTTCATCACTACAA 338
QY 47 -----LyleleugluSerSerGluProThrglnGlyLevalGluThrle 61
DB 339 CTACAGAAGGTGTAACTGAGAGAGTAAACATTAAATACCTTCTGAGAGAACATTT 398
QY 62 ThrAspGlyValThrlelyGlyVallySerGluLeuValGlyGluysProArgValal 81
DB 399 ATTGATGATCTGATAGG---ATCAGAGG-----AGGGGATC 434
QY 82 ProlySProglYAspGlyGluyslelyGlyuTleAspProThrleuysAspPheArg 101
DB 435 CCTCACCGGAGCTGGTGCAGAAAGTTTGAATAATGACCCCTTTGACAACTATCGT 494
QY 102 SerHisleuAspTyrArgTyrSerGluYrArgArgIleArgAlaAlaIleAspGlnHis 121
DB 495 CAACACCTTGATTTACAGGATTCACAGTACAGAAAGTGAAGGAGCAATTGACAACTAT 554
QY 122 GluGlyGlyLeuGlyValaPheSerArgGlyTyrGluYleuGlyPheThrArgSerAla 141
DB 555 GAGGGGTGTTGGAGCTTTTCTCGTGGTTATGAAAAATGGGTTTCACTCGATGCT 614

DB 615 AAGGTATCACTTACCGAGAGGAGCTCTGATGCCATGACGTCCTCATTTGAGAT 674
QY 162 PheAsnAsnTyrAspProAsnAlaAspThrMetThrArgAspAspTyrGlyValTyrGlu 181
DB 675 TTCAACAATTTGGAGCAAGATCTGACATTATGATCGGAAAGAAATTTGGTCTGGAG 734
QY 182 IlePheLeuProAsnAlaAspGlySerProAlaIleProHisGlySerArgValIys 201
DB 735 ATTTTTCGCCAAATATGATGATGTTCTCTGCAATTCCTCATGGTCAAGAG 794
QY 202 IleArgMetAspThrProSerGlyVallyAspSerIleSerAlaTyrIlelyPheSer 221
DB 795 ATACGTATGACACTCCATCAGATGTTTAAGATTCATTCCTGCTGGATCACTACTCT 854
QY 222 ValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProglugluGlu 241
DB 855 A--CAGCTTCGTAGTAATTCATTAATGAAATATATATGATCCACCCGAGAGAG 912
QY 242 LysTyrValPheGlnHisProGlnProlyArgProGlnSerleuArgIleTyrGluSer 261
DB 913 AGGTATATCTTCCAAACCCAGCGCCAAAGAAACCAAGTCTGTGAATATATGATCT 972
QY 262 HisIleGlyMetSerSerProgluProlyIleAsnSerTyrAlaAsnPheArgAspGlu 281
DB 973 CATATTTGAGATGATGATGCTCGAGCTTAATTAATTAATCACTACGATGATTTAGATGAA 1032
QY 282 ValLeuProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGlu 301
DB 1033 GTTCTTCCCTCGCAATAAAAGCTTGGTCAATGAGCTGCAAAATTATGGCTATTCAGAG 1092
QY 302 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAspPheAlaProSerSerArg 321
DB 1093 CATTTCTTATTAATGATGATGTTTGGTATCATGATCAAAATTTTGGCAAGAGACCGT 1152
QY 322 PheGlyThrProgluAspLeuLysSerleuIleAspArgAlaHisGluLeuGlyLeu 341
DB 1153 TTGGAAACCGCCAGACACCTTAAGTCTTTGATGATTAAGCTAGAGTATGATGTT 1212
QY 342 ValLeuMetAspIleValHisSerHisSerSerAsnAsnThrleuAspGlyLeuAsnGly 361
DB 1213 GTTCTCATGATCAATGTTTCAACCCATGACATCAAAATATCTTTAGATGATGATGATG 1272
QY 362 PheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisHisTyrMetTyr 381
DB 1273 TTGGAGCGCACCATGATGTTTCTTCACTCTGAGACTGCTGTTTATCATTTGATGAG 1332
QY 382 AspSerArgLeuPheAsnTyrGlySerTyrGluValleuArgPheLeuSerAsnAla 401
DB 1333 GATTTCCGCTTTTAACTATGAGAACTGGAGGATCTAGGTATCTCTCAAAATCG 1392
QY 402 ArgTyrTyrleuGluGlyTyrLysPheAspGlyPheArgPheAspGlyValThrSerMet 421
DB 1393 AGATGGGTGTGATGATGATCAATTTGATGATGATTTGATGATGATGATGATGATG 1452
QY 422 MetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyTyrPheGly 441
DB 1453 ATGTATACCAACACGAGATTTATCGGTGATTCCTGGAACCTAGAGAAATACCTTTGA 1512
QY 442 PheAlaThrAspValaAspAlaValaTyrleuMetLeuValaAspLeuIleHisGly 461
DB 1513 CTGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1572
QY 462 LeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIle 481
DB 1573 CTTTCCCAAGATGATTAATCATTTGATGATGATGATGATGATGATGATGATGATG 1632
QY 482 ProValProAspGlyGlyValGlyPheAspTyrArgLeuHisMetAlaValaAspLys 501
DB 1633 CCGCTTCAAGTGGGGGTGGCTTTTACATTCGCTGATATGCAATTCGATGATTA 1692
QY 502 TyrIleGluLeuLeuLysSerAspGluSerTyrIleAspIleValHisThr 521


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Db      1693  GCGATTGAGTTGCTCCAGAAACCGGATGAGATTGCAAGAGTGGGATATTGTTGATACA 1752
QY      522   LeuThrAsnaGArGTpLeuGluLysCysValThrTyrAlaGluSerHisAspGlnAla 541
Db      1753  CTGCAAAATATAAAGATGGTCCGGAAGAAAGTGTGTTGATATCGCTGAAGATCATATGAAAGT 1812
QY      542   LeuValGlyAspIleThrIleAlaPheThrLeuMetLysAspMetTyrAspPheMet 561
Db      1813  CTAGTCGGTGTAAACATATAGCATTTCCGCTGATGGAACAAGATATGATATATTTTATG 1872
QY      562   AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMetIle 581
Db      1873  GCTTCGATGATAGCCGCCAACATCATTAATAGATCGTGGGATGCAATTCGACAAAGATGANT 1932
QY      582   ArgLeuValThrMetGlyLeuGluGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 601
Db      1933  AGCGTTTGATTAATAGGATTTAGAGAGAGAAAGGGTACCTAAATTTTCATGGGAATAGATTC 1992
QY      602   GlyHisProGluTyrPLeuAspPheProArgGlyProGlnThrLeuProThrGlyLysVal 621
Db      1993  GGGCAACCCCTGGTGGATTTGATTTCCCTAGGGCTGAACAACACCTTCGATGACTCAGTA 2052
QY      622   LeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgPheAspLeuGlyAspAla 641
Db      2053  ATTCGCCGAAACCAATTTCAGTTATGATATAATGACACGAGATTTGACCTGGAGATGCA 2112
QY      642   AspPheLeuArgTyrHisGlyMetGlnLysPheAspGlnAlaMetGlnHisLeuGluGlu 661
Db      2113  GAAATATTTAAGATACCGTGGGTTCGAAAGATTTGACCGGGCTATGACAGATCTTGAAAT 2172
QY      662   LysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGluLysPheLys 681
Db      2173  AAAATATGAGTTTATGACTTCAGAACACAGTTCATATACGAAAGATGAAGAGATAG 2232
QY      682   ValIleIlePheGlnArgGlyAspLeuValPheValPheAsnPheHisTyrSerAsnSer 701
Db      2233  ATGATGTGATTTGAAAAAGAAACCTAGTTTGTCTTTAATTTTCATCTGAGCAAAAAC 2292
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QY      722   AsnAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrThrThrThr 741
Db      2353  GATGATCAACATTTTGTGTGGCTTCGCGAGAAATGATCATTAATGCCGAATATTTCACCTTT 2412
QY      742   GlnHisProHisAspAsnArgProArgSerPheSerValIleThrThrProSerArgThrAla 761
Db      2413  GAAAGAGATGATGATGATGCTCTCGTTCATATTAGTGTATGACACTTGTGTGAACAGCA 2472
QY      762   ValValTyrAlaLeuThrGlu 768
Db      2473  GTGCTCTATGCACTAGTAGAC 2493

RESULT 14
US-10-056-454A-18
; Sequence 18, Application US/10056454A
; Publication No. US20030166919A1
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unidigma Blvd.
CITY: Newcastile
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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[illegible]

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 QY 222 ValGlnAlaProGluGluLeuProPheAsnGlyIleTyrTyrAspProGluGluGlu 241
 Db 1161 TTACAGCTTCCTGATGAATTCATCATATATGAAATATATATGATCATCCACCGAAGAGAG 1220
 QY 242 LysTyrValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrGluSer 261
 Db 1221 AGGATGCTCTCCAAACACCAAGCCCAAGAAACCAAACTCGTGAATATATGATCT 1280
 QY 262 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGlu 281
 Db 1281 CATATTGAAATAGATAGTCCGAGCCTTAATTAATCTCATCGTAATTTTACAGATGAA 1340
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 Db 2001 TGGATTTAGTCTCTCAAGAAACGGGATGAGATGAGATGAGAGTGGTGTATATTTGTTACA 2060
 QY 522 LeuThrAsnArgArgTyrPheGluLysCysValThrTyrAlaGlnSerHisAspGlnAla 541
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RESULT 15
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 ? Sequence 337, Application US/0993842A
 ? Patent No. US20020160378A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Harper, Jeff
 ? APPLICANT: Kreps, Joel
 ? APPLICANT: Wang, Xun
 ? APPLICANT: Zhu, Hong
 ? TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ? FILE REFERENCE: SAME, AND METHODS OF USE
 ? CURRENT APPLICATION NUMBER: US/09/538,842A
 ? PRIOR FILING DATE: 2001-08-24
 ? PRIOR APPLICATION NUMBER: US 60/227,866
 ? PRIOR FILING DATE: 2000-08-24
 ? PRIOR APPLICATION NUMBER: US 60/264,647
 ? PRIOR FILING DATE: 2001-01-16
 ? PRIOR APPLICATION NUMBER: US 60/300,111
 ? PRIOR FILING DATE: 2001-06-22
 ? NUMBER OF SEQ ID NOS: 5379
 ? SEQ ID NO 337
 ? LENGTH: 2577
 ? TYPE: DNA
 ? ORGANISM: Arabidopsis thaliana
 ? US-09-538-842A-337

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 Pred. No.: 3155.00
 Score: 87.27%
 Percent Similarity: 87.27%
 Best Local Similarity: 75.20%
 Length: 2577
 Matches: 561
 Conservative: 90
 Mismatches: 79

Tue Apr 20 10:02:29 2004

us-09-508-377-12.rnpb

Page 22

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Job time : 665 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 17, 2004, 19:54:05 ; Search time 108 Seconds
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3946.317 Million cell updates/sec

Title: US-09-508-377-12
Perfect score: 4169
Sequence: 1 MATFANSGATLGVARRPAA.....PRSFVTPSRVAVYALTE 768

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Searched: 682709 seqs, 277475446 residues
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-VOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-DEF_TIMEOUT=120 -WARN_TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4031.5	96.7	2853	4	US-09-609-040-3 Sequence 3, Appl1
2	3588.5	86.1	2446	4	US-09-731-166-9 Sequence 9, Appl1
3	3351	80.4	2720	4	US-09-731-166-11 Sequence 11, Appl1
4	3342	80.2	2725	4	US-08-941-445A-14 Sequence 14, Appl1
5	3341	80.1	2665	4	US-09-557-894-1 Sequence 1, Appl1
6	3189	76.5	3074	4	US-09-087-277-1 Sequence 1, Appl1
7	3189	76.5	3074	4	US-09-658-499-1 Sequence 1, Appl1
8	2924	70.1	2087	4	US-09-257-894-9 Sequence 9, Appl1
9	2917	70.0	2165	4	US-09-257-894-8 Sequence 8, Appl1
10	2327	53.4	1393	4	US-09-087-277-3 Sequence 3, Appl1
11	2327	53.4	1393	4	US-09-658-499-3 Sequence 3, Appl1
12	2165.5	51.9	3128	3	US-08-716-449-1 Sequence 1, Appl1

13	2146	51.5	2470	4	US-09-731-166-13 Sequence 13, Appl1
14	2146	51.5	2487	4	US-09-257-894-19 Sequence 24, Appl1
15	2146	51.5	2565	4	US-09-257-894-24 Sequence 16, Appl1
16	2146	51.5	2763	3	US-08-941-445A-16 Sequence 12, Appl1
17	2146	51.5	2772	4	US-09-257-894-12 Sequence 1, Appl1
18	2115.5	50.7	2909	3	US-08-104-158-1 Sequence 1, Appl1
19	2115.5	50.7	2909	4	US-09-609-040-1 Sequence 25, Appl1
20	1586.5	40.5	1809	4	US-09-257-894-25 Sequence 29, Appl1
21	1586.5	40.5	1865	4	US-09-367-895-29 Sequence 29, Appl1
22	1542.5	37.0	11469	4	US-09-981-803-29 Sequence 29, Appl1
23	1542.5	37.0	11478	3	US-08-983-440-29 Sequence 194, Appl1
24	1542.5	37.0	11478	3	US-08-983-440-29 Sequence 1, Appl1
25	1520.5	36.5	5402	4	US-09-221-0178-194 Sequence 1, Appl1
26	559.5	13.8	2475	4	US-09-557-884-1 Sequence 1, Appl1
27	559.5	13.4	1830121	4	US-09-643-990A-1 Sequence 3960, Appl1
28	559.5	13.4	1830121	4	US-09-489-039A-3960 Sequence 1, Appl1
29	544.5	13.1	2307	4	US-09-537-120-1 Sequence 8197, Appl1
30	541.5	13.0	1866	4	US-09-252-991A-8197 Sequence 3, Appl1
31	535	12.8	2472	4	US-08-528-026C-3 Sequence 1, Appl1
32	528.5	12.7	2426	3	US-09-103-840A-1 Sequence 2, Appl1
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37	473	11.3	303	4	US-09-401-064-304 Sequence 8121, Appl1
38	448	10.7	601	4	US-08-961-527-45 Sequence 123, Appl1
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40	427.5	10.3	1308	4	US-08-311-731A-123 Sequence 8057, Appl1
41	325	7.8	36470	4	US-09-252-991A-8057 Sequence 14, Appl1
42	297	7.1	1770	4	US-09-252-991A-8057 Sequence 14, Appl1
43	297	7.1	1947	4	US-09-252-991A-8057 Sequence 14, Appl1
44	282.5	6.8	1680	3	US-09-242-690A-14 Sequence 14, Appl1
45	282.5	6.8	1680	4	US-09-908-855-14 Sequence 14, Appl1

ALIGNMENTS

RESULT 1
US-09-609-040-3
; Sequence 3, Application US/09609040
; Patent No. 6570066
; GENERAL INFORMATION:
; APPLICANT: Millimeter, et al.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE
; FILE REFERENCE: 514413-3515.1
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: PCT/EP92/00302
; PRIOR FILING DATE: 1992-02-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2853
; TYPE: DNA
; ORGANISM: Trilicium aestivum
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (313)..(2499)
; OTHER INFORMATION: BRANCHING ENZYME
US-09-609-040-3

Alignment Scores:
Pred. No.: 0
Score: 4031.50
Percent Similarity: 92.56%
Best Local Similarity: 91.46%
Query Match: 96.70%
DB: 4
Gaps: 1
Length: 2853
Matches: 750
Conservative: 9
Mismatches: 9
Indels: 52

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Dp	342	ATCTTCAGAACCGACTCAGGGCAATGTGGAAACATCACTAGTGTGTAAACAAAGGAT	401
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Qy	109	rgluTyraArgargIleargAlaAlaIleaspGlnHisgluGluGlyLeuGluAlaPheSe	129
Dp	522	CGAATPACAGAAATTCGTGCTGCTATTGACCACCATAGAGGTGATGGAGCAATTTTC	581
Qy	129	rArgGluTyrgluLysleuGlyPheThrArgSerAlaGluGlyIlethrTyraGluTr	149
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Dp	762	TGGATCCTCAGCTATTCTTCATGCTCAGTTCAGTAAAGATACGGAATGGATACCTCATCCGG	821
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Qy	249	nProLysArgProGluSerLeuArgIleTyrgluSerHisIleGlyMetSerSerProGlu	269
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Db	1842	ATTCTGGTTGATGATTAAGCATATGATGATATTTCACTGCTCGATAGGCTTCAACTCC	1901
Qy	569	oArgIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGly	589
Db	1902	TGCGAATGATCGGGCATAGCAATTAATAAATGATCAGGCTTGTCACCATGGGTTAAG	1961
Qy	589	yGlyGlyGluGlyTryLeuAsnPheMetGlyAsnGluPheGlyHisAspGluTrpIleAspPr	609
Db	1962	TGGTGAACCTATCTTAATCTTATGAGGAATAGATTGGAGCATCCGAAATGGATTAATTT	2021
Qy	609	eProArgGlyProGluThrLeuProThrGlyLysValLeuProGlyAsnHisAsnSerTry	629
Db	2022	TCCAAAGGCCCAAACTCTTCCAAACGGCAAAAGTTCCTCCGAAATPAACAATATATA	2081
Qy	629	rAspLysCysArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTrpHisGlyPhe	649
Db	2082	TGATAAATCCCGCGGTAGATTGATTTGGAGATGCAGAATTTCTTAAGATATGCTGATAT	2141
Qy	649	tGlnGluPheAspGlyAlaMetGlnHisLeuGluGluGluLysTryGlyPheMetThrSerGly	669
Db	2142	GCAAGGTTCGATCGACCATGACAGATCTTGAGGAAAAATATAGGTTTATGACATCTGA	2201
Qy	669	uHisGlnTryValSerArgLysHisGluGluAspLysValIleIlePheGluArgGlyHis	689
Db	2202	GCAACCGATATGTTTCCGGAACATAGAGAAATAGTGAATCATCTTTCGAAAGAGAGAGA	2261

QY 689 PleuValPheValPheAspPheHisTrpSerAsnSerPhePheAspTyrArgValGlyCys 709
Db 2262 TTGGATATTGTTTTCACCTGACCTGAGACCAATAGCTTTTTCATACCGTGTGGGTG 2321
QY 709 SerArgProGlyValTyrTyrValAlaLeuAspSerAspAlaLeuPheGlyGlyPhe 725
Db 2322 TTCACAGCTGGAGAGTACAGAGTGGCTTGACCTCGACAGATGCACTCTTGTGAT 2381
QY 729 SerArgLeuAspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgPro 749
Db 2382 CAGCAGCTGTGATCAAGATGCTGACCTACCTACCAACGAACTCCGATGACCAACAGGCC 2441
QY 749 ArgSerPheSerValTyrThrProSerArgThrAlaValTyrAlaLeuThrGlu 768
Db 2442 GCGCTCTTCTCGGTGTACCTCCGACAGAACTGCGGTGTGTATGCCCTTACAGAG 2499

RESULT 2

US-09-731-166-9
; Sequence 9, Application US/09731166
; Patent No. 6639126
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccharides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731,166
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,993
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2446
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: SBE11a
; OTHER INFORMATION: Genbank Accession No. 6639126 U65948
; NAME/KEY: CDS
; LOCATION: (2)...(2446)
US-09-731-166-9

Alignment Scores:

Pred. No.: 0 Length: 2446
Score: 3588.50 Matches: 662
Percent Similarity: 88.75% Conservative: 32
Best Local Similarity: 84.65% Mismatches: 49
Query Match: 86.08% Indels: 39
Gaps: 4

US-09-508-377-12 (1-768) x US-09-731-166-9 (1-2446)

QY 11 LeuGlyValAlaArgProAlaAlaAlaGlnProGluGluLeuGlnIleProGluAsp 30
Db 113 CTTCTCTCCGACAGCGCGTGGACACCTCAACCTGAGAGATACAGATCTCGAA--- 169
QY 31 TleGluGluGlnThrAlaGluValAsnMetThrGlyGlyThrAlaGluValLeuGluSer 50
Db 170 -----GCAGAACTG-----ACTGTGGAGAG---ACATCC 196
QY 51 SerGluProThrGln-----GlyIleValGluThrIleThrAsp 63
Db 197 TCTCTACCAACTCAACAAACATCATCAGCAGTGGCTGAAACCACTCAGAGCTGAG 256
QY 56 -----GlyIleValGluThrIleThrAsp 63
Db 257 GAGAGCGCTGAGCTCTCAGAAAGTATTGAGATTGAGAGTACTGTGAAACCAAAATTGAT 316
QY 64 GlyValThrIleGlyValIleGluLeuValValGlyGluValProArgValValProLys 83

Db 317 GGTGAGGATCAAAAGCAACCACTGCGAGAGAGAAACAGAGTTATCCACCA 376
QY 84 ProGlyAspGlyGlnIleTyrGluIleAspProThrLeuLysAspPheArgSerHis 103
Db 377 CCAGAGATGGCGCAACGAATATATAGATTGACCCCAATTTGGAGAGGTTTGGGGGTAC 436
QY 104 LeuAspTyrArgTyrSerGlyTyrArgArgIleArgAlaAlaIleAspGlnHisGlyGly 123
Db 437 CTGACTACCAATACAGTAATATAGATTAACGCGCGCTATTCATGATCAACATGAGGT 496
QY 124 GlyLeuGluAlaPheSerArgGlyTyrGluValLeuGluPheThrArgSerAlaGluGly 143
Db 497 GGTGTGATGCTTTTTCACGCGGTTCAGAAAGCTTGAGTTTACTGTCGACGCGCTGAAGGT 566
QY 144 IleThrTyrArgGluTyrAlaProGlyAlaHisSerAlaAlaLeuValGlyAspPheAsn 163
Db 557 ATCACTTACAGAGATGGGCTCTGAGCATCTCTGACGACATTGATGAGTGACTTCAAC 616
QY 164 AsnTrpAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTyrGluIlePhe 183
Db 617 AACTGAAACCAAAAGCTGATGCTATGGCCAGAAATGAGATACGCGCTTGGAGATTTC 676
QY 184 LeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIleArg 203
Db 677 CTGCTTAACAATGCTGATGATTCCTCTATTCCTCAAGCTCAGCTGTAAGATACG 736
QY 204 MetAspThrProSerGlyValLysAspSerIleSerAlaTyrIleLysPheSerValGln 223
Db 737 ATGACACACACATCTGCTGTATAGATTCCATTCCTGCTGATCAAGTTTCTGTGACG 796
QY 224 AlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGluGlyTyr 243
Db 797 GCTCCAGGTGAATCCATACCAACGCTATATATATATGACCCCACTTAAGAGGAATAT 856
QY 244 ValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrGluSerHisIle 263
Db 857 GTATTCAACACCTCAACCTTAAGCGGCCCAAGTCACTCGGATATATGATATCATGTT 916
QY 264 GlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGluValLeu 283
Db 917 GGAATGATTAAGCCCGGACCAAAAGTAATATACATATGTAACCTGACAGATGAGGTCT 976
QY 284 ProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGluHisSer 303
Db 977 CCAGAAATTAATAAAGCTTGATGATACATGCAATGCAATATGCAATCCAGAAACCTCT 1036
QY 304 TyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGly 323
Db 1037 TATTATGCAAGCTTGGTACCATGTTACGAATTTTGGCCCAAGTACCGCTTTGGG 1096
QY 324 ThrProGluAspLeuLysSerLeuIleAspArgAlaHisGlyLeuGlyLeuValLeu 343
Db 1097 ACTCCAGAGGACCTAAATCTCTTATGATAAAGCCATGAGCTTGCTGATGCTCT 1156
QY 344 MetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAsp 363
Db 1157 ATGATATATGTTCAATAGCTTCAATCAATCAATTAATACCTTGATGATGTTGATG 1216
QY 364 GlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisIleThrMetTyrAspSer 383
Db 1217 GGCACGATACATTACTTCAATGATGATCCAGAGCCATATGATGATGATGATCT 1276
QY 384 ArgLeuPheAsnTyrGlySerTyrGluValLeuArgPheLeuLeuSerAsnAlaArgTyr 403
Db 1277 CGCTATTCATTAATGAGGAGTTGGAAAGTTTGAATTTCTATTTGCAATGCGAGATG 1336
QY 404 TrpLeuGluGluTyrLysPheAspGlyPheArgPheAspGlyValHisSerMetMetTyr 423
Db 1337 TGGCTTGAAGAAATATAAATTTATGATGATTTGATGAGGGGTGACCTCCATGATATAT 1396
QY 424 ThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyValLysTyrPheGlyPheAla 443
Db 1397 ACTCAACATGATTAACAATGATCACTCTGGAACATAAGCAATATTTTGAATTTGCC 1456

QY 193 AlaIleProHISGlySerArgValIlysIleArgMetAspThrProSerGlyValIyAsp 212
 Db CCTATTCTCAAGGAGTCTGTTAAAGGTGAAGATGATCTCACTCAGGATTAAGGAT 829
 QY 213 SerIleSerAlaTriIleIyPheSerValGlnAlaProGlyGluIleProPheAsnGly 232
 Db TCATATCCAGCCTGGATCAAGTACTCAGTCCAGCCCGAGAGAAATACCATGTAGTGG 889
 QY 233 IleTyrTyrAspProGluGluGluIyTyrValPheGlnHisProGluIleProIyAsp 252
 Db ATTTATTATGATCTCTCGTCAAGAGTAAAGTATGTCTTCAGCATGGCAACCTTAAACGA 949
 QY 253 ProGluSerIleuArgIleTyrGluSerHisIleGlyMetSerSerProGluProIySile 272
 Db CCAAAATCATTCGGATATATGAACAACATGTGGAATGATGCCCGAACCAGACATA 1009
 QY 273 AsnSerTyrAlaAsnPheArgAspGluValIleuProArgIleuYsArgIleuGlyTyrAsn 292
 Db AACACATATGTAACTTTAGGATGAAAGTCTCCCAAGATTAATAAAACCTTGATCAAT 1069
 QY 293 AlaValGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisVal 312
 Db GCAGTGCATATATGGCAATCCCAAGAGCACTCATATATGAAAGCTTTGGATTCATGTA 1129
 QY 313 ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeuYsSerIle 332
 Db ACTTAATTTTTTGGCCAGATAGTCTGTTTGGTACCCCAAGAGATGAAGTCTTTGATT 1189
 QY 333 AspArgAlaHisGluIleuGlyLeuValIleuMetAspIleValHisSerHisSerSer 352
 Db GATAGAGCAATAGAGCTGTTGTTGCTAGTCTCATGATGTGGTTCATAGCATGACGCCA 1249
 QY 353 AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly 372
 Db AGTAATACTCTGGATGGTGTGAATGTTTGTATGTGTACAGATACACATTACTTTCACAGT 1309
 QY 373 GlyProArgGlyHisHisStrMetTrpAspSerArgPheAsnTyrGlySerTrpGlu 392
 Db GGTCACGGTGGCCATCATCTGATGTGGATTTCTGCCATATTTAACTATGGAACTGGGA 1369
 QY 393 ValIleuArgPheLeuSerAsnAlaArgTyrTrpLeuGluGluIyTyrYsPheAspGly 412
 Db GTTTTAAAGATTCTTCTCTCCAAATGATAGTGGTCCGAGAAATTAAGTTTGAATGT 1429
 QY 413 PheArgPheAspGlyValIleuSerMetMetTyrThrHisGlyLeuGluMetThrPhe 432
 Db TTCCTGTTTGTAGTGGTGGACCTCATATGATACACTCATCCGAGATTAACAAGTAACTTT 1489
 QY 433 ThrGlyAsnTyrGlyGluIyTyrPheGlyPheAlaHisPheValAspAlaValIleu 452
 Db ACGGGAACTTCAATGATTTGGCTTGGCCACCGATGATGATGACAGTGGTTTACTTG 1549
 QY 453 MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGluAsp 472
 Db ATGCTGTTAAATGATCTTAATTCATGACTTATCTGAGGCTGATTAACCATTTGATGAAT 1609
 QY 473 ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr 492
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 QY 493 ArgLeuHisMetAlaValAlaAspIleStrIleGluLeuLeuYsGluSerAspGluSer 512
 Db CGAGTGAATGCTGCTGCTGACCAATGATGATGATCTTCCAGCAAGTATTAAT 1729
 QY 513 TrpIyMetGlyAspIleValHisHisThrLeuThrAsnArgTyrTrpLeuGluIyCysVal 532
 Db TGGAAAGATGGGTATATTGTGCACACATGCAAAATAGAGAGTGTAGAAAGTGTGA 1789
 QY 533 ThrTyrAlaGluSerHisAspGlnAlaLeuValGlyAspIyStrIleAlaPheThrPhe 552
 Db ACTATGCTGAAAGTCAATGATCAAGCATTAAGTCCGCAACAACATTAATGCCGTTTGGTGG 1849

QY 553 MetAspIyAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
 Db ATGGAACAAGATATGATATGATTTATGATGCTCCCTCGATTAACCTTCAACTCCATGAT 1909
 QY 573 ArgGlyIleAlaLeuHisIleYsMetIleArgLeuValThrMetGlyLeuGlyGluGly 592
 Db CGTGGATAGCATTAACATTAAGATGATTAGCTTACATCAATGGGTTTAGAGAGAGGGC 1969
 QY 593 TyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluIleIleAspPheProArgGly 612
 Db TATCTTAATTTCAATCGGAAATGAAGTTTGACATCTGATATGATATTTCCAAAGGT 2029
 QY 613 ProGlnThrLeuProThrGlyIyValIleuProGlyAsnAsnAsnSerTyrAspIyCys 632
 Db CCGCAAGACTTCCAAAGTGAAGTTTATTCAGGGAATTAACAACAGTTATGACAAATGT 2089
 QY 633 ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnIyPhe 652
 Db CGTGAAGATTTGACCTGGTGAATGACAGCTATCTTATGATATCATGTATGCAAGCTT 2149
 QY 653 AspGlnAlaMetGlnHisLeuGluGluIyTyrGlyPheMetThrSerGluHisGlnTyr 672
 Db GATCAGGCAATGCAACATCTTGAGCAAAATTAATGATCATGATCATCTGATCACCAAGTAT 2209
 QY 673 ValSerArgIyHisGluGluAspIyValIleIlePheGluArgGlyAspLeuValPhe 692
 Db ATTTCCCGAAACATGAGAGAGATTAAGTATGTTGTAAGAAAGAGATTTGGATTT 2269
 QY 693 ValPheAsnPheHisStrSerAsnSerPheAspTyrArgValGlyCysSerArgPro 712
 Db GTGTCAACTTCCACTGCAACAACGCTATTTTGACTTACCGATATGTGTTCCAAAGCTT 2329
 QY 713 GlyIyTyrIyValAlaLeuAspSerAspAlaLeuPheGlyGlyPheSerArgLeu 732
 Db GGGGTATATAGTGTGTGTGATCTCCAGCGGTGACATTTGTGGATTTTACAGAGAT 2389
 QY 733 AspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgProArgSerPhe 752
 Db CATCACGACGCCGACACTTCCCGCCGCTGTCAGATGATATAGCCATATTCATTC 2449
 QY 753 SerValTyrThrProSerArgThrAlaValIleTyrAlaLeuThrGlu 768
 Db TCGGTTTAAACCAAGCAAGACATGTGTGCTATGCTCCAGTGAAG 2497

RESULT 4
 US-08-941-445A-14
 ; Sequence 14, Application US/08941445A
 ; Patent No. 6107060
 ; GENERAL INFORMATION:
 ; APPLICANT: Keeling, Peter
 ; APPLICANT: Guan, Hanning
 ; TITLE OF INVENTION: Starch Encapsulation
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS: Winner and Sullivan, P.C.
 ; STREET: 5370 Manhattan Circle
 ; CITY: Boulder
 ; STATE: CO
 ; COUNTRY: US
 ; ZIP: 80303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/941,445A
 ; FILING DATE: 30-SEP-1997
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/026,855
 ; FILING DATE: 30-SEP-1996
 ; INVENTOR:

```

NAME: Winster, Ellen P
REGISTRATION NUMBER: 26,547
REFERENCE/DOCKET NUMBER: 868
TELECOMMUNICATION INFORMATION
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2725 base pairs
TYPE: nucleic acid
STANDARDS: single
TOPOLOGY: not relevant
MOLECULE TYPE: mRNA
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 91..264
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 265..2487
FEATURE:
NAME/KEY: CDS
LOCATION: 91..2490
OS-08-941-445A-14

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Db 1780 ATTATGCTGAAGATGATGATCAAGCATTTGCGGCAAGACTATTGGCTTTGTTG 1839
Qy 553 MetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
Db 1840 ATGCACAAAGATATGATGATTTCAAGCCCTCGATGAGACTTCAACTCCACGATTGAT 1899
Qy 573 ArgGlyTAlaLeuHisLysMetCLeaArgLeuValThreGlyLeuGlyGlyGly 592
Db 1900 CCGGATGACATTACATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1959
Qy 593 TyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGly 612
Db 1960 TATCTTAATTTCTAGGGAATGAGTTTGACATCTCTGAATGATGATGATGATGATGAT 2019
Qy 613 ProGlnThrLeuProThrGlyLysValLeuProGlyAsnAsnAsnSerTyrAspLysCys 632
Db 2020 CCGCAAGACTTCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2079
Qy 633 ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnLysPhe 652
Db 2080 CGTCGAAGATTGACCTGGGTGATGACAGACTATCTTGGTATCATGCTTATGCAAGAGTTT 2139
Qy 653 AspGlnAlaMetGlnHisLeuGluGluLysTyrGlyPheMetThrSerGluHisGlnTyr 672
Db 2140 GATCAGGCAATGCAACATCTTGAGCAAAATATGAAATTCATGACATCTGATCACAGTAT 2199
Qy 673 ValSerArgLysHisGluGluAspLysValIleIlePheGluArgGlyAspLeuValPhe 692
Db 2200 ATTCCCGGAACATGAGGAGGATTAAGTATGATGATGATGATGATGATGATGATGATGAT 2259
Qy 693 ValPheAsnPheHisTyrSerAsnSerPhePheAspTyrArgValGlyCysSerArgPro 712
Db 2260 GTGTTCAACTTCCACGCAACAGCTATTTTGACTTACCTGATGCTTGGTTCGCAAACTT 2319
Qy 713 GlyLysTyrLysValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeu 732
Db 2320 GGGGGGTAAAGGTGCTTGGAGCTCGACGCTGAGACTATTTGGTGAATTTAGAGGATC 2379
Qy 733 AspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgProArgSerPhe 752
Db 2380 CATCAGCAGCGAGAGACTTCAACCGCGAGCTGTCGATGATATAATAGCCATATTCATTC 2439
Qy 753 SerValTyrThrProSerArgThrAlaValValTyrAlaLeuThrGlu 768
Db 2440 TCGGTTTATACACAGAGACATGTCGTCTATGCTCCAGTGGAG 2487

RESULT 5
US-09-257-894-1
Sequence 1, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0a

APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 79..2476
US-09-257-894-1
Alignment Scores:
Pred. No.: 0 Length: 2665
Score: 3341.00 Matches: 608
Percent Similarity: 86.98% Conservative: 67
Best Local Similarity: 78.35% Mismatches: 79
Query Match: 80.14% Indels: 22
Gaps: 4
US-09-508-377-12 (1-768) x US-09-257-894-1 (1-2665)
Qy 4 PheAlaValSerGlyAlaThrLeuGlyVal-----AlaArgProProAla 18
Db 181 TTCTTAATCGGGGTGCTCGAATTGATTTGGGGAGCCGACGCGGCTATCGCGGCGG 240
Qy 19 AlaAlaGlnProGluGluLeuGlnIleProGluAspIleGluGlnThrAlaGluVal 38
Db 241 GCCGGCGCAGAGAGCGCGTATGTTCTGAGGGCGAAGATGAT----- 285
Qy 39 AsnMetThrGlyGlyThrAlaGluLysLeuGluSerSerGlu----- 52
Db 286 -----GGCTCCGACCAAGGGCTGACTCGGCTCAATTCAGTCGATGACTG 333
Qy 53 ProThrGlnGlyIleValGluThrIleThrAspGlyValThrLysGlyValLysGluLeu 72
Db 334 GAGGTACCAACATTTCTGAGAGACACACGCTGCGGTCT-----GCTGCTGATGCT 387
Qy 73 ValValGlyGluLysProArgValValProLysProGlyAspGlyGluLysIleTyrGlu 92
Db 388 CAAAGCTTGAACAGAGTTGAGTGTCTCCCGCCACCAAGAGATGACAAAATATTCAG 447
Qy 93 IleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGlyTyrArg 112
Db 448 ATTTGACCCCATGTTGCAAGGCTATTAAGTACCTCTTGAATATCGTACAGCTCTTAGA 507
Qy 113 ArgIleArgAlaAlaIleAspGlnHisGluGlyGlyLeuGluAlaPheSerArgGlyTyr 132
Db 508 AGAATCCCTTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
Qy 133 GluLysLeuGlyPheThrArgSerAlaGluGlyIleThrTyrArgGluTrpAlaProGly 152
Db 568 GAGAAGTTTGATTTAATGCCAGCGCGAAGGATACATATGAGAAATGGGCTCTCGGA 627
Qy 153 AlaHisSerAlaAlaLeuValGlyAspPheAsnAsnTrpAsnProAsnAlaAspMet 172
Db 628 GCATTTTCTGAGCATTTGTTGGTGTACTTCAACACTGGGATCCAAATCCAGATCGTATG 687
Qy 173 ThrArgAspAspTyrGlyValIleProGluIlePheLeuProAsnAsnAlaAspGlySerPro 192

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QY 193 AAlaIleProhIseRgIseRgVAllysIleArgWetAspThrProSerGlyValIlyAsp 212
Db 748 CCAATTCCTCATGATGATCTGCTGTAAGGTAGATGATGATCTCATGCGGATTAAGGAT 807
QY 213 SerIleSerAlaTrpIleYsPheSerValGlnAlaProGlyGluIleProPheAsnGly 232
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QY 233 IleTYrTYrAspProPheProGluGluIlyTYrValPheGlnHisProGluProIlyAsn 252
Db 868 ATTATATATATATCTCTGAAAGAGGTAAAGTATGTGTTCAGGATGGCAACCTTAAGCA 927
QY 253 ProGluSerLeuArgIleTYrGluSerHisIleGlyMetSerSerProGluProIlyAsn 272
Db 928 CCAAAATCATGTCGGATATATGAAACATGTCGGAATGAGTAGCCCGAAACCGAAGATA 987
QY 273 AsnSerTYrAlaAsnPheArgAspGluValLeuProArgIleYsArgLeuGlyTYrAsn 292
Db 988 AACACATATGTAAACTTTAGGAGTGAAGTCTCTCCCAAGATTAATAAACTTGATACAT 1047
QY 293 AlaValGlnIleMetAlaIleGlnGlnHisSerTYrTYrAlaSerPheGlyTYrHisVal 312
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QY 333 AspArgAlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer 352
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QY 373 GlyProArgGlyHisIleTYrMetTrpAspSerArgLeuPheAsnIlySerIlyProGlu 392
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QY 393 ValLeuArgPheLeuLeuSerAsnAlaArgTYrTrpLeuGluGluTYrIlyPheAspGly 412
Db 1348 GTTTTAAATTTCTCTCTCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
QY 413 PheArgPheAspGlyValThrSerMetTYrThrHisIleGlyLeuGlnMetThrPhe 432
Db 1408 TTCGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1467
QY 433 ThrGlyAsnTYrGlyGluTYrPheGlyPheAlaThrAspValAspAlaValIlyLeu 452
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QY 453 MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGluAsp 472
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QY 513 TrpIlyMetGlyAspIleValHisTrpLeuThrAsnArgTrpLeuGluIlyCysVal 532
Db 1708 TCGAAGATGATGATATTTGTCACACATGCAAAATGAGGAGGTATGAGAGAGTGTGTA 1767
QY 533 ThrTYrAlaGluSerHisAspGlnAlaLeuValGlyAspIlyThrIleAlaPheTrpLeu 552

QY 553 MetAspIlyAspMetTYrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
Db 1828 ATGACCAAGGATATATGATATTCATGAGCTCTGATGATGATGATGATGATGATGATGAT 1887
QY 573 ArgGlyIleAlaLeuHisIlySerMetIleArgLeuValThrMetGlyLeuGlyGlyGly 592
Db 1888 CCGGATATGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1947
QY 593 TYrLeuAsnPheMetGlyAsnGluPheGlyHisProGluIlyTrpIleAspPheProArgGly 612
Db 1948 TATCTTAATTTATGATGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2007
QY 613 ProGlnThrLeuProThrGlyIlyValLeuProGluYAsnAsnAsnSerTYrAspIlyCys 632
Db 2008 CCGCAAAAGCTTCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2067
QY 633 ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTYrHisGlyMetGlnIlyPhe 652
Db 2068 CCGTCAAGATTTGACCTGGGTGATGACATCTTATGATCATGATGATGATGATGATGAT 2127
QY 653 AspGlnAlaMetGlnHisLeuGluGluIlySTyGlyPheMetThrSerGluHisGlnTYr 672
Db 2128 GATCAGGCAATGCAACATCTTGAGCAAAATATGAAATTCATGATGATGATGATGATGAT 2187
QY 673 ValSerArgIlyHisGluGluAspIlyValIleIlePheGluArgGlyAspLeuValPhe 692
Db 2188 ATTTCCCGAAGATATGAGAGATTAAGTATGTGTTCGAAAGAGATTTGTATTT 2247
QY 693 ValPheAsnPheHisTrpSerAsnSerPhePheAspTYrArgValGlyCysSerArgPro 712
Db 2248 GTTTCATCTTCACATGCAACAACAGCTATTTGATGATGATGATGATGATGATGATGAT 2307
QY 713 GlyIlySTyIlyValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeu 732
Db 2308 GGGGTATATAGGTGTCCTTGACTCGACGCTGAGTATTTGATGATGATGATGATGATGAT 2367
QY 733 AspHisAspValAspIlyPheThrThrGluHisProHisAspAsnArgProArgSerPhe 752
Db 2368 CATCAGCAGCCGACGACTTACCGCGGACTGTTCGATGATGATGATGATGATGATGAT 2427
QY 753 SerValTYrThrProSerArgThrAlaValIlyValIlyAlaLeuThrGlu 768
Db 2428 TCGGTTATATACCAAGCAAGACATGTGTCTATGCTCCAGTGAG 2475

RESULT 6
US-09-087-277-1
Sequence 1, Application US/09087277B
Patent No. 6169226
GENERAL INFORMATION:
APPLICANT: EK, BO
APPLICANT: KHOSNODI, Jamshid
APPLICANT: LARSSON, Claes-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087, 277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: bell gene

OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
FEATURE:
NAME/KEY: CDS
LOCATION: (189) ..(2825)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (189) ..(332)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (333) ..(2825)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (92) ..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
OTHER INFORMATION: n wherein n = A, C, G or T.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (285) ..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
OTHER INFORMATION: or Phe.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1405) ..(1406)
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1428) ..(1430)
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1896) ..(1898)
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2154) ..(2156)
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-087-277-1
Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 3189.00 Matches: 585
Percent Similarity: 82.78% Conservative: 83
Best Local Similarity: 72.49% Mismatches: 91
Query Match: 76.49% Indels: 48
DB: 3 Gaps: 6
US-09-508-377-12 (1-768) X US-09-087-277-1 (1-3074)
QY 2 AlaThrPheAlaValSerGlyAlaThrLeu-----GlyValAlaArgProProAlaAla 19
DB 366 TCTACAGTTGACGACATCGGGAAAGTCTTGCTGCGTGAACCCAGAGTAGATGCTCTCA 425
QY 20 AlaGlnProGluGluLeuGlnIleProGlu----- 29
DB 426 TCCCTACAGCCCAATTGATGATTCACATCTCCAGAAATTCCCGACATCACT 485
QY 30 AsPIleGluGluGlnThrAlaGlu----- 37
DB 486 GATGTRGATGATTCACAAATGGAACGCTAGGACATTTAAACTGAGAACGATGACGTT 545
QY 38 -----ValAsnMetThrGlyGlyThrAlaGlu----- 46
DB 546 GAGCCGTCAAGTATCTTACAGAGAGTGTGAAGAGCTGATTTTGCTTCATCACTACAA 605
QY 47 -----LysLeuGluSerSerGluProThrGlnGlyIleValGluThrIle 61
DB 606 CTACAGAAAGGTGCTAACTGAGAGAGTCTAAACATTAATACCTTCTGAAGAGACAAAT 665
QY 62 ThrAspGlyValThrLysGlyValLysGluLeuValValGlyGluLysProArgValVal 81
DB 666 ATTGATGATCTGATAGG---ATCAGAGAG-----AGGGGAGATC 701

QY 82 ProLysProGluYAspGlyGlnLysIleTyrGluIleAspProThrLeuYAspPheArg 101
DB CCTCCACCTGACCTTGCTCAGAAAGATTATGAATAAGACCCCTTTGCAACATCTGCT 761
QY 102 SerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAlaIleAspGlnHis 121
DB CAACACCTTGATTAAGGATTACAGATCAAGAACTAGAGGAGGACATTAAGCAAGTAT 821
QY 122 GluGlyGlyLeuGluAlaPheSerArgIlyTyrGluLysLeuGlyPheThrArgSerAla 141
DB GAGGTGGTTGGAGGCTTTTCTCGTGGTTATGAAAAATGGGTTTCACTCGTAGTGCT 881
QY 142 GluGlyIleThrTyrArgGluTPrAlaProGlyAlaHisSerAlaAlaLeuValGlyAsp 161
DB ACAGGTATCACTTACCGTAGAGGGCTCCTGGTGGCCAGTCCCTCCATCTGAGAT 941
QY 162 PheAsnAsnTPrAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValITPrGlu 181
DB TTCAACAATTGGAGCGCAATGCTGACATTATGACTCGGAATGATTTGGTCTGGAG 1001
QY 942 TTTTTCGCCAATAATATGTGATGTTCTCTGGCAATTCCTCATGCTCAGAGTGAAG 1061
QY 182 IlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValLys 201
DB ATTTTTCGCCAATAATATGTGATGTTCTCTGGCAATTCCTCATGCTCAGAGTGAAG 1061
QY 202 IleArgMetAspThrProSerGlyValLysAspSerIleSerAlaTrpIleLysPheSer 221
DB ATACGTATGACACCTCCATCAGGTGTAAAGATTCATCTCGCTTGATCACTACTCT 1121
QY 1062 ValGlnAlaProGluGluIleProPheAsnGlyIleTyrTyrAspProProGluGlu 241
DB TTAACGCTCTCGATGAATTCATATATGAAATATATATGATCACCACGAGAGAG 1181
QY 1122 LysTyrValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrGluSer 261
DB AGGTATATCTTCACAAACCCAGCGCAAGAACCAACAAATCCCTGAGATATGTGATCT 1241
QY 1182 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGlu 281
DB CATATGGAATGAGTAGTCCGAGCGCTAAATTAATCTCATGATGATTTTAAAGATGAA 1301
QY 1242 ValLeuProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGlu 301
DB GTCCTCTCGATGAATAAGCTTGAGTACATGCGGTCGCAATTTGGCTATTCAAGAG 1361
QY 1302 CATCTTATTTANGCATAGTTTGTTGTTATCATGTCACAAATTTTTCACACCAACACCGT 1421
QY 302 PheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeu 341
DB TTTGGAACNCCCGACGACCTTAAGCTTTGATGATTAAGCTCATGATGATGAAATGTT 1481
QY 342 ValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGly 361
DB GTTCTCATGACATTTGTTCAACGCCATGATCAATTAATACCTTAGATGACCTGAACATG 1541
QY 362 PheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisIleStrpMetTrp 381
DB TTTGACGCGACAGATAGTTGTTACTTTCACCTGAGAGCTCGTGGTATCATGATGATG 1601
QY 1542 AspSerArgLeuPheAsnTyrGlySerTrpGluValIleArgPheLeuSerAsnAla 401
DB GATTCGCCCTCTTTAACTATAGAAACCTGGAGGAPCTTAAGATATTTCTCTCAAAATGCG 1661
QY 402 ArgTrpTrpLeuGluGluTyrLysPheAspGlyPheArgPheAspGlyValThrSerMet 421
DB AGATGGTGTTGATGATGATTCAAATTTGATGATTTAGATTTGATGATGATGATCAATG 1721
QY 1662 MetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGlyTyrPheGly 441
DB ATGATATCTACCAACGAGATTATCGGTGGATTCACCTGGGAACTACGAGAGAAATCTTTGGA 1781

QY 30 Aspl1eglulgluInThrAlaglu----- 37
 Db 486 GATGTAGATGATGTCACACATGGAACAGCTAAGCAGATTAAACTGAGAAAGATGAGCT 545
 QY 38 -----ValasMetHrglyglYThraAlaglu----- 46
 Db 546 GAGCCGCTCAAGTGATCTTACAGGAAGGTGGAAGAGCTGATTTGCTTCACTACTACAA 605
 QY 47 -----LysLeuGlusSerSerGlubProHrgInglyl1eValGlulThr1le 61
 Db 606 CTACAAAGAGGTGTAACCTGAGAGAGCTTAAACATTAAATACTCTTGAGAGACAACT 665
 QY 62 ThrAspGlyVal1ThrlYsglyVal1LysgluLeuVal1GlulglulYsProArgVal1Val 81
 Db 666 ATTGATGATCTGATAG---ATCAGAGAG-----AGGGGCATC 701
 QY 82 ProLysProGlyYAspGlyglulYs1leTyrglu1leAspProThrlLeuLysAspPheArg 101
 Db 702 CCTCCACCTGAGACTTGGTGAGGAAGATTATGAATAAGACCCCTTTGACAACTATGCT 761
 QY 102 SerHisLeuAspTyrrArgTyrrSerGluTyrrArgArg1leArgAlaAla1leAspGlnHis 121
 Db 762 CAACACCTTGATTAACAGTATTCACAGTACAGAACTGAGGAGGACAAATTGACAGATAT 821
 QY 122 GluGlyglYleuGlu1u1aPheSerArgGlyTyrglu1u1LysLeuGlyPheThrArgSerAla 141
 Db 822 GAGGGGCTTTGGAAGCTTTTCTCGTGGTTATGAAAAATGGSTTTCACTCGTAGTCT 881
 QY 142 GluGly1leThrTyrrArgGlu1u1rPal1aProGlyAlaHisSerAlaAla1leuVal1GlyAsp 161
 Db 882 ACAGGATACACTTAACGCTGAGTGGGCTCGTGCCAGTCAAGCTGCCCTCATTTGAGAT 941
 QY 162 PheAsnAsnTyrAsnProAsnAlaAspThrMetThrArgAspAspTyrrGlyVal1ITrglu 181
 Db 942 TTCAAATAATGGAGCCAAATGCTGACATTATATGCTGGAAATGATTTGGTGTGGAG 1001
 QY 182 1lePheLeuProAsnAsnAlaAspGlySerProAla1leProHisGlySerArgVal1Lys 201
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 QY 202 1leArgMetAspThrProSerGlyVal1LysAspSer1leSerAla1leATrP1leLysPheSer 221
 Db 1062 ATAAGTATGAGACACTCATCAGATGTTAAGATTCATTCCTGCTTGATCAACTACTCT 1121
 QY 222 ValGlnAlaProGlyglul1leProPheAsnGly1leTyrrTyrrAspProProGluGlu 241
 Db 1122 TTAACACTTCTCGATATAATATTCATATATATGATATATATATATATATATATATAT 1181
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 Db 1182 AGGTATATCTTCCAAACACCCAGCCCAAGAAACCAAGATGCTGAGAAATATATATATCT 1241
 QY 262 His1leGlyMetSerSerProGluProLys1leAsnSerTyrrAlaAsnPheArgAspGlu 281
 Db 1242 CATATGAGATGATGATGATCCGAGGCTTAAATTAATCATCATCGAATTTTAAAGATGAA 1301
 QY 282 Val1leuProArg1leLysArgLeuGlyTyrrAsnAlaValGln1leMetAla1leGlnGlu 301
 Db 1302 GTTCTTCCCGCAATAAAAGCTGGGTGATACATGCGGTGCATAATTAATGCTATTCAGAG 1361
 QY 302 HisSerTyrrTyrrAlaSerPheGlyTyrrHisVal1ThraPhePheAlaProSerSerArg 321
 Db 1362 CATCTCTATATATGCTATTTGTTGATATCATGTCGAATTTTNGACACCAAGACCGCT 1421
 QY 322 PheGlyThrProGluAspLeuLysSerLeu1leAspArgAlaHisGluLeuGlyLeuLeu 341
 Db 1422 TTTGGAACCCCGACGACCTTAAGTCTTGAATGATATGATGATGAGCTGAGATTTGTT 1481
 QY 342 Val1leuMetAsp1leVal1HisSerHisSerSerAsnAsnThrlLeuAspGlyLeuAsnGly 361
 Db 1482 GTTCTATGAGCATGTTCACAGCCATGACATCAATATATATCTTAAAGATGAGCTAAACATG 1541

QY 362 PheAspGlyThrAspThrHisTyrrPheHisGlyglYProArgGlyHis1leStrPmetTrp 381
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 Db 1602 GATTCGCCCTCTTTAACTATGAAACCTGGAGGCTCTTAAGTATCTTCTCAAAATGCG 1661
 QY 402 ArgTrpTrpLeuGluGluTyrrLysPheAspGlyPheArgPheAspGlyVal1ThrSerMet 421
 Db 1662 AGATGCTGTGGATGAGTCAAAATTTGATGATTTGATGATGATGATGATGATGATGATG 1721
 QY 422 MetTyrrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrglyglYTyrrPheGly 441
 Db 1722 ATGTATCTCACACAGATATACGGAGGATTCACCTGGAACCTACAGAGATATCTTTGGA 1781
 QY 442 PheAlaThrAspVal1AspAlaVal1TyrrLeuMetLeuVal1AsnAspLeu1leHisGly 461
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 QY 462 LeuHisProAspAlaVal1Ser1leGlyglYAspVal1SerGlyMetProThrPheCys1le 481
 Db 1842 CTTTCCAGATGCAATTAACATGTGTGAAGATGTTAGCGGAATGCCGACATTTTATTT 1901
 QY 482 ProVal1ProAspGlyglYVal1GlyPheAspTyrrArgLeuHisMetAlaVal1aAspLys 501
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 QY 502 Trp1leGluLeuLeuLysGlnSerAspGluSerTyrrLysMetGlyAsp1leVal1HisThr 521
 Db 1962 TGGATTTGAGTTGCTCAAGAAACGGATGAGATTGGAGAGTGGGATATATTTGCTATACA 2021
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 Db 2022 CTGACAAATAGAAAGATGTCGGAAAGTGTGTTCTAGCTGAAAGTCAATGATCAAGCT 2081
 QY 542 LeuVal1GlyAspTyrrThr1leAlaPheTrpLeuMetAspLysAspMetTyrrAspPheMet 561
 Db 2082 CTAGCGGATGATTAACATATATGATCTTCCGCTGATGAGAAAGATATATATATTTATG 2141
 QY 562 AlaLeuAspArgProSerThrProArg1leAspArgGly1leAlaLeuHisLysMet1le 581
 Db 2142 GCTCGATAGAACCTTCAACATCATTAATATAGATCGGATAGCATTGACACAGATGAT 2201
 QY 582 ArgLeuVal1ThrMetGlyLeuGlyglYTyrrLeuAsnPheMetGlyAsnGluPhe 601
 Db 2202 AGGCTTGTAACATATGATGATGAGAGAGAGGATATCTAAATTTCAATGGAAATGAATTC 2261
 QY 602 GlyHisProGluTyrr1leAspPheProArgGlyProGlnThrLeuProThrglyLysVal 621
 Db 2262 GGCACCTGAGTGAATGATTTCCCTAGGCTGAAACCAACCTCTCTGATGGCTCAGTA 2321
 QY 622 LeuProGlyAsnAsnAsnSerTyrrAspLysCysArgArgArgPheAspLeuGlyAspAla 641
 Db 2322 ATTCGCCGAAACCAATTCAGTATGATATAATCAGACGAGATTTTGAACCTGGAGATGCA 2381
 QY 642 AspPheLeuArgTyrrHisGlyMetGlnLysPheAspGlnAlaMetGlnHisLeuGluGlu 661
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 QY 662 LysTyrglyPheMetThrSerGluHisGlnTyrrVal1SerArgGlyHisGluGluAspLys 681
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 QY 682 Val1le1lePheGlnLysArg1leAspLeuVal1PheVal1PheAsnPheHis1leTrpSerAsnSer 701
 Db 2502 ATGATTTGATTTGAAAAAGAAACCTTAATTTTGTCTTAATTTTCACTGGAACAAAAAGC 2561
 QY 702 PhePheAspTyrrArgVal1GlyCysSerArgProGlyLysTyrrLysVal1aLeuAspSer 721
 Db 2562 TATTCAGCTATGCAATGAGCTGCTGAGACCTGGAAGATTCAGAGGTGCTTGACTCA 2621
 QY 722 AspAspAlaLeuPheGlyglYLysSerArgLysAspHisAspVal1AspTyrrPheThrThr 741


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1210 GATCCAGCTGGCCATCATCTGAGTGGGATTCCTGCTATTACTATGGAAGTGGGAA 1269
393 ValLeuArgPheLeuLeuSerAsnAlaArgTrpLeuGluGluTrpLeuPheAspGly 412
1270 GTTTTAAGATTCTCTCTCCCAATGCTAGTGGTGGCTGAGGAATATAAGTTGATGCT 1329
413 PheArgPheAspGlyValThrSerMetMetCysTrpHisHisGlyLeuGlnMetTrpPhe 432
1330 TTCCCTTTTGAGTGGTGTGACCTCCCAAGATGATGACACACACGCAATTAACAGTAACATT 1389
433 ThrGlyAsnTrpGlyGluTrpPheGlyPheAlaThrAspValAlaValAlaValTrpLeu 452
1390 ACGGGGAACCTCAATGAGTATTTTGGCTTTGGCCACGAGTGTAGTCAAGTGTACTTG 1449
453 MetLeuValAsnAspLeuLeuHisGlyLeuHisProAspAlaValSerIleGlyGluAsp 472
1450 ATGCTGGTAAAGATGATTAATTCATGACCTTATCCTGAGGCTGTAACCATTTGGTGAAGAT 1509
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1510 GTTAGTGGATGCTCATTTGGCTTCCCTGTTCAAGATGTTGGGTGATTTTGCTAT 1569
493 ArgLeuHisMetAlaValAlaAspTrpIleGluLeuLeuGlnSerAspGluSer 512
1570 CGGATGCATATGGCTGTGGCTGCAATGATGATGATTCCTCAAGCAAGTGAATGAAGT 1629
513 TrpLeuMetGlyAspIleValHisThrLeuThrAsnArgTrpLeuGluGlyCysVal 532
1630 TCGAAGATGGTGTGATTTGTGGTGCACACTGACAAATAGAGGTGTAGAGAGTGTGTA 1689
533 ThrTrpAlaGluSerHisAspGlnAlaLeuValGlyAspTrpTrpIleAlaPheTrpLeu 552
1690 ACTTATGCTGAAGAATCATGATCAAGCATTAAGTCGGGCAAGCATTAATGGCTTTGGTGT 1749
553 MetAspIleAspMetTrpAspPheMetAlaLeuAspArgProSerTrpProAspIleAsp 572
1750 ATGGACCAAGATATGATGATTTTCATGAGCCCTCGATAGACCTTCACCTCACCATTGAT 1809
573 ArgGlyIleAlaLeuHisIleAspMetIleArgLeuValThrMetGlyLeuGlyGluGly 592
1810 CGTGGGATAGCATTAACATAAGATGATTAAGCTTATCACTATGAGTTTGAAGAGAGGCG 1869
593 TyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGly 612
1870 TATCTTAATTTTCATGGGAATGAGTTTGGACATCCTGAATGATGATGATTTTCCAAAGAGT 1929
613 ProGlnThrLeuProThrGlyValValLeuProGlyAsnAsnAsnSerTrpAspGlyCys 632
1930 CCGCAAGACCTTCCCAAGTGTATGATTATTCAGGGGATTAACAACACTTATGAACAAATGT 1989
633 ArgGlyArgPheAspLeuGlyAspAlaAspPheLeuArgTrpHisGlyMetGlnGluPhe 652
1990 CGTCAAGATTTGACCTGGGTGATGCAAGTATCTTATGATATCATGTTATGCAAGAGATTT 2049
653 AspGlnAlaMetGlnHisLeuGluGluGlyLeuTrp 663
2050 GATCAGGCAATGCAACATCTTGAGCAAAATAAT 2082

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ADDRESSER: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
FAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-257-894-8
Alignment Scores:
Pred. No.: 6,55e-316 Length: 2165
Score: 2917.00 Matches: 532
Percent Similarity: 87.48% Conservative: 55
Best Local Similarity: 79.28% Mismatches: 62
Query Match: 69.97% Indels: 22
Gaps: 4
US-09-508-377-12 (1-768) x US-09-257-894-8 (1-2165)
4 PheAlaValSerGlyAlaThrLeuGlyVal-----AlaArgProProAla 18
1985 TTCTTAATCTGGGGGCTCGAATGATGATGTTGCGGAGCAGCAGGGGCTATGCGGGCGG 1926
19 AlaAlaGlnProGluGluGlnLeuGlnLeuProGluAspIleGluGluGlnThrAlaGluVal 38
1925 GCCGGCGCCAGAGAGCGGTGATGTTCTGAGGCGGAGAAATGAT-----1881
39 AsnMetThrGlyGlyThrAlaGluLeuGlnSerGlu-----52
1880 -----GGCTCGGACATCAAGGGGTGACTCGGCTCAATTCCAGTCGATGAACCTG 1833
53 ProThrGlnGlyIleValGluThrIleThrAspGlyValThrLyseGlyValGlyGluLeu 72
1832 GAGGTACAGACATTTCTGAGAGACAAACGTGCGGTCT-----GATGGCTGATGCT 1779
73 ValValGlyGluValProArgValAlaProLysProGlyAspGlyGlnIleTrpGlu 92
1778 CAAGCTTGAACAGAGTTCGAGTGTCCCCCAACAGAGGATGAGCAAAATAATTCAG 1719
93 IleAspProThrLeuLeuAspPheArgSerHisLeuAspTrpArgTrpSerGlyTrpArg 112
1718 ATTGACCCCATGTTGCAAGGCTATAGTACATCTTGAATTCGATGACGCTCTATAGA 1659
113 ArgIleArgAlaAlaIleAspGlnHisGlyGlyValGluGluAlaPheSerArgGlyTrp 132
1658 AGAATCCGTTGACATGATGATTAACATGAAAGAGGCTTGGAAAGCTTCTCCGATGAT 1599
133 GluTrpLeuGlyPheThrArgSerAlaGluGlyIleThrTrpArgGluTrpAlaProGly 152

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RESULT 9
US-09-257-894-8/c
Sequence 8, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Brogile, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS

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Db	1538	GCATTTTCTGCAGCATTTGTGGGTGACGTCACAACATCGGATCCAAATGCAGATCGATG	1479
Qy	173	ThrArgAspAspTyrGlyValTrpGluLeuPheLeuProAsnAsnAlaAspGlySerPro	192
Db	1478	AGCAAAATGGTGGTGGTGGTGGAAATTTTCTGCTTAACAATGCAGATGGATCAACA	1419
Qy	193	AlaIleProHisGlySerArgValIleValIleArgMetAspTrpProSerGlyValIleAsp	212
Db	1418	CCATTTCTCATGGATCTCGGTGAATAGGTGAGATGATACCTCATCCAGGATTAAGAT	1359
Qy	213	SerIleSerAlaTrpIleLeuAspPheSerValGlnAlaProGlyGluIleProPheAsnGly	232
Db	1358	TCAATTCAGCGCTGGATCAAGTACTCAATGCAGGCGCCAGGAGAAATACCATATGATGG	1289
Qy	233	IleIleTyrTrpAspProProGluGluGluLysTyrValPheGlnHisProGlnProLysArg	252
Db	1298	ATTATATATATGATCTCTCCGAAGAGATTAAGTATGTTCCAGCATCGCCAACTPAACGA	1239
Qy	253	ProGluSerIleAspGlyLeTyrGluSerHisIleGlyMetSerSerProGluProLysIle	272
Db	1238	CCAAATTCATTGGGATATATGAAACAATGTCCGAATGATGACCCGGAAACGAAGATA	1179
Qy	273	AsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsn	292
Db	1178	AACACATATGTAACCTTAGGAGATGAATCTCTCCCAAGATTAATAAACTTGATACAT	1119
Qy	293	AlaValGlnIleMetAlaIleGlnGlnHisSerTyrTyrAlaSerPheGlyTyrHisVal	312
Db	1118	GCAGTGCAAATTAATGGCATCCAGAGACCTCATATTAAGAACTTTGGATACCAATGA	1059
Qy	313	ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIle	332
Db	1058	ACTATATTTTGTGGCCCAAGTATGCTTTGTGTAACCCAGAAAGATTGAATCTTTGAT	999
Qy	333	AspArgAlaHisGlyLeuGlyLeuLeuValLeuValIleValHisSerHisSerSer	352
Db	998	GATGAGACACATGAGCTTGTTGCTAATGTCATGATGTGGTTCATATGACATGACGCTCA	939
Qy	353	AsnAsnThrIleuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly	372
Db	938	AGTATATCTCGAGATGGGTGAATGGTTTATGTGTAACATGACATACCATTTCTTCACGT	879
Qy	373	GlyProArgGlyHisHisIleTrpMetTrpAspSerArgLeuPheAsnTyrGlySerTrpGlu	392
Db	878	GGTCCACGTGGCCATCACTGGATGTGGGATTTCTGCGCATTTTAATAAGGAACTGGAA	819
Qy	393	ValLeuArgPheLeuLeuSerAsnAlaArgTrpIleuGluGlyTyrLysPheAspGly	412
Db	818	GTTTAAATATTTCTCTCTCCATGCTGATGAGTGCGCTCGAGGATATTAAGTTGATGGT	759
Qy	413	PheArgPheAspGlyValIleThrSerMetMetTyrThrHisGlyLeuGlyMetThrPhe	432
Db	758	TTCCGTTTGAATGGGTGACCTCCATGATGTACACTCACACGAGATTCAAGTAACTATT	699
Qy	433	ThrGlyAsnTyrGlyGluTyrPheGlyPheAlaThrAspValAspAlaValValTyrIleu	452
Db	698	ACGGGAACTTCAATGAGATATTTTGGCTTTCGCCACCGATGTAGATGCGATGTTACTTG	639
Qy	453	MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGluAsp	472
Db	638	ATGCTGGTAATGATCTAATTCATGACTTTATCTGTAGCGCTGTAACCATTTGGTAAAT	579
Qy	473	ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr	492
Db	578	GTTATGGAAATGCCATACATTTGGCCCTTCTGTTCAAGATGGGTGGATTTGACAT	519
Qy	493	ArgLeuHisMetValAlaValAspLysTrpIleGluLeuLeuLysGlnSerAspGluSer	512

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Db      518 CGGATGCATATGGCTGTGGCTGCAAAATGAGATTGACCTTCTCCAGCAAAAGTATGA
Qy      513 TTPlysmetGlyAspIleValHisThrLeuThrAsnaArgATPLeuGluIuIyCySVal
Db      458 TGGAAAGATGGGTGATATGTGTCCACACATGCAAAATAGAGGTGGTTAGAGAGTGTGT
Qy      533 ThrTyraGluSerHisAspGlnAlaLeuValGlyAspIlySThrIleAlaPheTrpLe
Db      398 ACTTATGCTGAAGACGATGATCAAGCATTAAGTCGGCGCAAGACTATAGCCGTTGGTT
Qy      553 MetAspIlyAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAs
Db      338 ATGGCAAGAGATATGATGATTTTCATGGCCCTCGATATACCTTCGAACCTCCATG
Qy      573 ArgGlyIleAlaLeuHisLeuMetIleArgLeuValThrMetGlyLeuGlyGluGlu
Db      278 CGTGGGATAGCATTAACATTAAGATGATTGATTCATCAAAATGGGTTTGGAGAGAGGG
Qy      593 TyrlleuAspPheMetGlyAsnGluIuPheGlyHisProGluTTPileAspPheProArgG
Db      218 TATCTTAATTTTCATGGGAATAGAGTTTGCAATCTGATGATGATGATTTTCCAGAGGG
Qy      613 ProGlnThrLeuProThrGlyIlyValLeuProGlyAsnAsnAsnSerTyrAspIlyCy
Db      158 CCGGAAGACTTCCAAAGTGAATGATTATTCGAGGAATTAACAACAGTTATGACAAATG
Qy      633 ArgArgArgPheLeuAspLeuGlyAspAlaAspPheLeuAlaGlyTrHisGlyMetGlnIuP
Db      98 CGTGAAGATTTTGACCTGGGTGAAGCACTATCTTATGATCATGATGATGCAAGAGTT
Qy      653 AspGlnAlaMetGlnHisLeuGluGluIuIySThr 663
Db      38 GATCAGGCAATGCACAACATCTTGAGCAAAATAT 6

RESULT 10
US-09-087-277-3
; Sequence 3, Application US/09087277B
; Patent No. 6,169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:bell gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.

```

T	459
1	532
A	399
U	552
G	339
P	572
T	279
Y	592
C	219
Y	612
T	159
S	632
T	99
e	652
T	39

NAME/KEY: misc.feature
LOCATION: (422)..(424)
OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
FEATURE:
NAME/KEY: misc.feature
LOCATION: (690)..(692)
OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1148)..(1150)
OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-087-277-3

Alignment Scores:
Pred. No.: 5,06e-239 Length: 1393
Score: 2227.00 Matches: 400
Percent Similarity: 93.09% Conservative: 31
Best Local Similarity: 86.39% Mismatches: 32
Query Match: 53.42% Indels: 0
Gaps: 0

US-09-508-377-12 (1-768) x US-09-087-277-3 (1-1393)

QY 184 LeuproAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIleArg 203
Db 2 CIGCCAAATATGATGGATGGTCTCCGCAATTCCTCATGGGTCAGAGTGAAGATACGT 61
QY 204 MetAspThrProSerGlyValIleAspSerIleSerIleThrIleLeuSerValGln 223
Db 62 ATGGACATCCCATCGAGGTGTAAGATTCATTCCTCTGGATCACTCATCTTTACAG 121
QY 224 AlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGluGluTyr 243
Db 122 CTTCCTGATGAATTCATATATGATATATATATATATATATATATATATATATATAT 181
QY 244 ValPheGlnHisProGlnProIleProIleProIleProIleProIleProIleProIle 263
Db 182 AACTTCACCAACCCAGCCGCAAGAAACCAAGATCGCTGAGATATATGATTCATAT 241
QY 264 GlyMetSerSerProGluProIleProIleProIleProIleProIleProIleProIle 283
Db 242 GGATATAGTAGTCCGAGGCTTAATAATTAATTAATTAATTAATTAATTAATTAATTA 301
QY 284 ProArgIleLeuArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGluHisSer 303
Db 302 CTTGCGTAAAAAGCTGGGTGATCAATGCGGTCAATTTATGGTATTTCAAGACATTTCT 361
QY 304 TyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGly 323
Db 362 TATTATGATAGTTTGGTATATCATGTCACAAATTTTTCGACCAACAGCCGTTTGA 421
QY 324 ThrProGluAspLeuIleSerIleIleAspArgIleHisGluGluGluValLeu 343
Db 422 ACNCCCGACGACCTTAACTTTGATGATTAAGCTAGCTAGGATGATGTTCTTC 481
QY 344 MetAspIleValHisSerHisSerSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAsp 363
Db 482 ATGGACATTTGTCACACCATGATCATCAATATATCTTTAGTGAATGACATGTTTAC 541
QY 364 GlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisIleTyrMetTyrAspSer 383
Db 542 GGCACAGATAGTGTACTTCACTCTGAGAGCTGCTGATTCATTTGATGATGAGATTC 601
QY 384 ArgLeuPheAsnTyrGlySerTyrGluValLeuArgPheLeuLeuSerAsnAlaArgTyr 403
Db 602 CGCTCTTTACTAGTGAAGCTGGAGGCTTGAATGATTTCTTCTCAAAAGCGAGATGG 661
QY 404 TrpLeuGluGluTyrIlePheAspGlyPheArgPheAspGlyValIleSerMetMetTyr 423
Db 662 TGGTTGATGATGATCAAAATTTGATGATTTGATTTGATTTGATTTGATTTGATTTGAT 721
QY 424 ThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGluTyrPheGlyPheAla 443

Db 722 ACTCACCGAGTATTCGGTGGATTCAGTGGAGTACAGAGAAATCTTTGATCTGCA 781
QY 444 ThrAspValAspAlaValIleTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuHis 463
Db 782 ACTGATGTCAGTCTGCTGTTGATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 841
QY 464 ProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIleProVal 483
Db 842 CCAGATGCAATTAACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 901
QY 484 ProAspGlyValIleGlyPheAspTyrArgLeuHisMetAlaValIleAspIleTyrIle 503
Db 902 CAGATGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
QY 504 GluLeuLeuGlySerAspGluSerTyrPlyMetGlyAspIleValHisThrLeuThr 523
Db 962 GAGTTGCTCAAGAAACGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1021
QY 524 AsnArgArgTyrPheGluGlyCysValThrTyrIleGluSerHisAspGlnAlaLeuVal 543
Db 1022 AATAGAAAGTGGTCGAAAGGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 1081
QY 544 GlyAspIleThrIleAlaPheThrPheMetAspIleAspMetTyrAspPheMetAlaLeu 563
Db 1082 GGTATTAACATATGATTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1141
QY 564 AspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisIleCysMetIleArgLeu 583
Db 1142 GATGACATTCATCAATCAT 1201
QY 584 ValThrMetGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyHis 603
Db 1202 GTAACTATGCGATTTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1261
QY 604 ProGluTyrIleAspPheProArgGlyProGlnThrLeuProThrGlyIleValLeuPro 623
Db 1262 CTTGCTGATGATGATTTCCCTGAGGCTGAACACACCTCTCTGATGCTGATGATTTCCC 1321
QY 624 GlyAsnAsnAsnSerTyrAspIleCysArgArgPheAspLeuGlyAspAlaAspPhe 643
Db 1322 GGAACCAATTAAGTATGATTAATGACAGCGAGTTTGAATCTGGAGATGAGATAT 1381
QY 644 LeuArgTyr 646
Db 1382 TTAAGATAC 1390

RESULT 11
US-09-658-499-3
Sequence 3, Application US/09658499
Patent No. 6469231
GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNODI, Jamshid
APPLICANT: LARSSON, Claes-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/658, 499
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087, 277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SB96/01558
PRIOR FILING DATE: 1996-11-28
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1393

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TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: beil gene fragment
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
NAME/KEY: CDS
LOCATION: (2)..(1393)
NAME/KEY: misc_feature
LOCATION: (424)..(1150)
OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
OTHER INFORMATION: C, G or T.
NAME/KEY: misc_feature
LOCATION: (422)..(424)
OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
NAME/KEY: misc_feature
LOCATION: (890)..(892)
OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
NAME/KEY: misc_feature
LOCATION: (1148)..(1150)
OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-508-499-3

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Alignment Scores:
Pred. No.: 5 066-239 Length: 1393
Score: 2227.00 Matches: 400
Percent Similarity: 93.09% Conservative: 31
Best Local Similarity: 86.39% Mismatches: 32
Query Match: 53.42% Indels: 0
Gaps: 0
US-09-508-377-12 (1-768) x US-09-658-499-3 (1-1393)

```

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QY 184 LeuProAsnAsnAlaAspGlySerProAlaIleProHISGlySerArgValIleArg 203
DB 2 CTGCAATATATATGATGGATGTTCTCTCTCAATCTCTCAATGGGTCCAGAGTGAAGATACGT 61
QY 204 MetAspThrProSerGlyValIleAspSerIleSerAlaTIPileSerPheValGln 223
DB 62 ATGACACCTCCATCAGGTGTTAAGATTCATCTCTGCTGATCACTACTCTTACAG 121
QY 224 AlaProGlyIleIleProPheAsnGlyIleTyrTyrAspProGluGluGlyTyr 243
DB 122 CTTCCTGATGAATTCATATATATGAAATATATATATATATATATATATATATATATATAT 181
QY 244 ValPheGlnHisProGlnProIleAspProGluSerIleArgIleTyrGlnSerHisIle 263
DB 182 ATCTTCCACACCCAGCGCCAAAGAACCAAGTGGCTGAGATATATATATATATATATATAT 241
QY 264 GlyMetSerSerProGluProIleAsnSerTyrTyrAlaAsnPheArgSpGluValIleu 283
DB 242 GGAATGATAGTCCGAGCGCTTAAATTAATCACTCAATGTAATTTAGAGATGAAGTCTT 301
QY 284 ProArgIleIleAspArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGlnHisSer 303
DB 302 CCGGCAATAAAGAGCTGGTACAAATGCGGTGCAAAATTTAGGCTTTCAGAGCATTTCT 361
QY 304 TyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGly 323
DB 362 TATATGCTAGATTGGTATCATGTCACAAATTTTTCGACCAAGACGCGCTTTTGAA 421
QY 324 ThrProGluAspLeuIleSerIleuIleAspArgAlaHisGlnIleuIleuValIleu 343
DB 422 ACNCCCGAGACTTAAGCTTTGATTGATTAAGCTTCATGAGCTAGAGATTTGTTCTC 481
QY 344 MetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAsp 363
DB 482 ATGACATTTGTCACAGCATGATCAATATATATATATATATATATATATATATATATAT 541
QY 364 GlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisIleTyrPheTyrPheSer 383
DB 542 GGCACAGATAGTGTGTTACTTCTGAGAGCTCGTGGTATATCATGATGATGAGATTC 601

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QY 384 ArgLeuPheAsnTyrGlySerTyrPglValIleuArgPheLeuLeuSerAsnAlaArgTyr 403
DB 602 CCGCTCTTAACTATAGGAAGACTGGAGGACTTAAAGTATCTTCTCAATGCGAGATGG 661
QY 404 TyrLeuGluGlyTyrIlePheAspGlyPheArgPheAspGlyValThrSerMetMetTyr 423
DB 662 TGGTTCATGATGATCAAAATTTGATGATTTAGATTTGATGATGATGATGATGATGAT 721
QY 424 ThrHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGlyTyrPheGlyPheAla 443
DB 722 ACTCACCGAGATTTGCGGTGGATTCACCTGGGAACTTACAGAGAAATCTTTGACCTGCA 781
QY 444 ThrAspValAspAlaValIleTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuHis 463
DB 782 ACTGATGATGATGCTGTTGATATCTGATGATGCTGCAACGATCTTATTCATGGGCTTTC 841
QY 464 ProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIleProVal 483
DB 842 CCAGATGCATTAACCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 901
QY 484 ProAspGlyValIleGlyPheAspTyrArgLeuHisMetAlaValAlaAspIleTyrIle 503
DB 902 CAAGATGGGGGTGTTGGCTTTGATCTATCGGCTCATATGCGCAATTCCTGATTAATGAT 961
QY 504 GluLeuLeuGlyGlnSerAspGluSerTyrPheMetGlyAspIleValHisThrLeuThr 523
DB 962 GAGTTCCTCAAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1021
QY 524 AsnArgArgTyrPheGluGlyCysValThrTyrAlaGluSerHisAspGlnAlaLeuVal 543
DB 1022 AATAGAGATGCGCGAAAGGTGTTCTATGCTGATGATGATGATGATGATGATGATGAT 1081
QY 544 GlyAspIleThrIleAlaPheTyrPheMetAspIleAspMetTyrAspPheMetAlaLeu 563
DB 1082 GGTGATTAACATTAATCATTTCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1141
QY 564 AspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisIleMetIleArgLeu 583
DB 1142 GATAGACNTCAACATCATATATATATATATATATATATATATATATATATATATAT 1201
QY 584 ValThrMetGlyLeuGlyGlyGlyTyrTyrLeuAsnPheMetGlyAsnGluPheGlyHis 603
DB 1202 GATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1261
QY 604 ProGluThrIleAspPheProArgGlyProGluThrIleuProThrGlyLeuValLeuPro 623
DB 1262 CCGAGTGGATTAATTTCTTAGGGCTGAACACACCTCTCTGATGCTGATGATGCTC 1321
QY 624 GlyAsnAsnAsnSerTyrAspIleCysArgArgIlePheAspLeuGlyAspAlaAspPhe 643
DB 1322 GGAACCAATTCATGATTAATGATTAATGATGATGATGATGATGATGATGATGATGAT 1381
QY 644 LeuArgTyr 646
DB 1382 TTAAGATAC 1390

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RESULT 12

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US-08-716-449-1
Sequence 1, Application US/08716449
Patent No. 6103893
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment
APPLICANT: Holding Corporation
TITLE OF INVENTION: Method for Producing Altered Starch
TITLE OF INVENTION: from Potato Plants
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott & Aylen
STREET: Box 194, 24th Floor, Toronto-Dominion Bank Tower
CITY: Toronto
STATE: Canada M5K 1H6
COUNTRY: Canada

```


QY 426 HisGlyLeuGlnMetThrPheMetGlyAsnTyrglyGluTyrrPheGlyPheAlaThrAsp 445
 : : : : :
 Db 1358 CATGGAAATCAATATGGAATTTACAGGAACCTAATATGATGTTTTCAGGAGCTTCAAT 1417
 QY 446 ValAspAlaValAlaTyrrLeuMetLeuValAsnAspLeuIleHisGlyLeuHisProAsp 465
 : : : : :
 Db 1418 GTTGAATCTGTGTCATTTATTTATGTTGGCCAAATATCTGATTCACAAATTTTCCCAAG 1477
 QY 466 AlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIleProValProAsp 485
 : : : : :
 Db 1478 GCAACTGTATATGCCGAAGATGTTTCTGTATGCGGGGCTTACGCGGCTGTCTTGAG 1537
 QY 486 GlyGlyValGlyPheAspTyrrArgLeuHisMetAlaValAlaAspLysTrpIleGluLeu 505
 : : : : :
 Db 1538 GGAAGAAATGGTTTGTATTTACCGCTGGCAATGGCAATCCAGATAAAGTGAATATAT 1597
 QY 506 LeuLys---GlnSerAspGlnSerTrpLysMetGlyAspIleValHisThrLeuThrAsn 524
 : : : : :
 Db 1598 TTAAAGATATAGATGATGAAGATTGTCATGAAGAAAGTAACTGCAATTCACAAAT 1657
 QY 525 ArgArgTrpLeuGlyGlyCysValThrTyrrAlaGlnSerHisAspGlnAlaLeuValGly 544
 : : : : :
 Db 1658 AGGAGATATACAGAGAGATGTATAGCATATGGGAGAGCCATGATCATGCTATGTGGGT 1717
 QY 545 AspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrrAspPheMetAlaLeuAsp 564
 : : : : :
 Db 1718 GACAAAGACATTTGATTTCTCTTAATGACAAAGAGATGATTTCTGGCATGTCCTTG 1777
 QY 565 ArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuVal 584
 : : : : :
 Db 1778 ACAATGCTTCTCTGTTGTGATGAGAAATGGCGTTCAACAATGATTCATTTTTC 1837
 QY 585 ThrMetGlyLeuGlyGlyGlyGlyTyrrLeuAsnPheMetGlyAsnGlnPheGlyHisPro 604
 : : : : :
 Db 1838 ACAATGGCTTGGGAGAGAGGGTAACTCAATTTCAATGGTAAAGAGTTGGCCATCT 1897
 QY 605 GlnTrpIleAspPheProArgGlyProGlnThrLeuProThrGlyLysValLeuProGly 624
 : : : : :
 Db 1898 GAGTGGATTTGACTTCTCTAGA-----GAGGAC 1924
 QY 625 AsnAsnAsnSerTyrrAspLysCysArgArgAspPheAspLeuGlyAspAlaAspPheLeu 644
 : : : : :
 Db 1925 AATTAATTTGAGTTATGACAAATGTAAGCCCACTGCAAGTCCGAGATGCGCAACTTG 1984
 QY 645 ArgTyrrHisGlyMetGlnGlnPheAspGlnAlaMetGlnHisLeuGlnGlyTyrgly 664
 : : : : :
 Db 1985 AGATTCAGATTTATGATGATCATTTGATAGAGCTATGAATTCGCTCATGAAAAAGTTCTCA 2044
 QY 665 PheMetThrSerGlnHisGlnTyrrValSerArgLysHisGlnGluAspLysValIleIle 684
 : : : : :
 Db 2045 TTCTCCCGCATCAGAAAAACAGATAGACACATGATGATGAATAGATGATGTTGTTG 2104
 QY 685 PheGlnArgGlyAspLeuValPheValPheAsnPheHisTrpSerAsnSerPhePheAsp 704
 : : : : :
 Db 2105 TTTGAACCTGTGACCTGTAATTTGATTTCACTTCCACCAATTAACATACATGCAAGGG 2164
 QY 705 TyrrArgValGlyCysSerArgProGlyLysTyrrLysValAlaLeuAspSerAspAla 724
 : : : : :
 Db 2165 TATAAAGTTGATGATGACTTTCAGGAGAGTACAGAGTTGCACTGGGCGATGCTTG 2224
 QY 725 LeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrrPheThrThr----- 741
 : : : : :
 Db 2225 GAATTTGGTGCCATGGAAGACCTGTCATGATGATGATTCATTCATTCATCAACAGAAAGA 2284
 QY 742 -----GlnHisProHisAspAsnArgProArgSerPheSerValTyrrThr 756
 : : : : :
 Db 2285 ATACCTGAGTTCACAAACAATTTCAATGTCGTCCAAATTCCTTCAAAAGTGCCTCT 2344
 QY 757 ProSerArgThrAlaValValTyrr 764
 : : : : :
 Db 2345 CTGCGCGCAACATGTTGGCTTAT 2368

US-09-731-166-13
 / Sequence 13, Application US/09731166
 / Patent No. 6639126
 / GENERAL INFORMATION:
 / APPLICANT: Sewalt, Vincent J. H.
 / APPLICANT: Singletary, George W.
 / TITLE OF INVENTION: Production of Modified Polysaccharides
 / FILE REFERENCE: 35718/206348
 / CURRENT APPLICATION NUMBER: US/09/731,166
 / PRIOR FILING DATE: 2000-12-06
 / PRIOR APPLICATION NUMBER: 60/169,993
 / NUMBER OF SEQ ID NOS: 16
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 13
 / LENGTH: 2470
 / TYPE: DNA
 / ORGANISM: Zea mays
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (0)..(0)
 / OTHER INFORMATION: SBE1 -- Genbank Accession No. 6639126 217959
 / NAME/KEY: CDS
 / LOCATION: (2)...(2470)
 / US-09-731-166-13
 Alignment Scores:
 Pred. No.: 1,52e-229 Length: 2470
 Score: 2146.00 Matches: 395
 Percent Similarity: 71.57% Conservative: 101
 Best Local Similarity: 57.00% Mismatches: 171
 Query Match: 51.48% Indels: 26
 DB: Gaps: 6
 US-09-508-377-12 (1-768) x US-09-731-166-13 (1-2470)
 QY 86 AspGlyGlnLysIleTyrrGluIleAspProThrLeuLysAspPheArgSerHisLeuAsp 105
 : : : : :
 Db 239 GACCATCTCCCAATTAATGATTCAGAGCAAGATGATTCAGAGACATTTCAAG 298
 QY 106 TyrrArgTyrrSerGlyTyrrArgArgIleArgAlaIleAspGlnHisGlyGlyLeu 125
 : : : : :
 Db 299 TACCGATGAAGAAAGATTCCTTAAGACAGAGAAAGATCAATTAAGAAATGAGGAAAGTCTT 358
 QY 126 GlnAlaPheSerArgGlyTyrrGlyLysLeuGlyPheThrArgSerAlaGlnGlyIleThr 145
 : : : : :
 Db 359 GAATCTTTTCTTAAGAGCTATTTGMAATTTGGGATTATATCAAAATGAGAGTGAATCTGTA 418
 QY 146 TyrrArgGlnTrpAlaProGlyAlaHisSerAlaIleValGlyAspPheAsnAsnTrp 165
 : : : : :
 Db 419 TATCGTAATAGGGACCTGCTGCGCAGAGGCAAGCTTATTTGTAATGACTG 478
 QY 166 AsnProAsnAlaAspThrMetThrArgAspAspTyrrGlyValTrpGluIlePheLeuPro 185
 : : : : :
 Db 479 AATGTCACAAACCTAATAGATGAGAGAGATTAATTTGGTGTGGTGCATCAAAATTT 535
 QY 186 AsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIleArgMetAsp 205
 : : : : :
 Db 536 GACCATGTCAAAGGAAACCTGCAATCCCTCAACATTCCAAAGTTAAATTTGGCTTTCTA 595
 QY 206 ThrProSerGlyValLysAspSerIleSerAlaTrpIleLysPheSerValGlnAlaPro 225
 : : : : :
 Db 596 CAGGTGGAAGTATGGGTGATGCGATTCACACATTTGATTCGTATAGCACTGTATGTC 655
 QY 226 GlyGluIle-----ProPheAsnGlyIleTyrrTyrrAspProProGlnGluGlyLysTyrr 243
 : : : : :
 Db 656 TCTAAATTTGAGAGCTCCCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715
 QY 244 ValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrrGlnSerHisIle 263
 : : : : :
 Db 716 ACATTTAAGATCTCTGGCTTCAAAAGCTTCTCTCCAGGATATCTATGAAAGCCATGTA 775

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Db      776 GGTATAGTGTGAAAAAGCCAGCAGTAAGCACAATATGAGGAAATTGACAGAAATGTGTG 835
Qy      284 Prox11LeuysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnIleHisSer 303
Db      836 CACGGCATACGACAAATTAATACACACAGTTGATGAGGATGATGAGGATGCG 895
Qy      304 TTTTAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGly 323
Db      896 TACTAGCTCTTCTGGGTACCATGTGACAAATTTCTTGGGTAGCAGACATCAGGC 955
Qy      324 ThrProGlnAspLeuPheLeuLeuLeuLeuLeuLeuLeuLeuValLeu 343
Db      956 ACACCCAGAGGACCTCAAAATCTGTTGATAGGCACACAGTTTGGGTTTGGAGTTCTG 1015
Qy      344 MetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAsp 363
Db      1016 ATGAGATGTTGTCATACGACATGACAGTAATATCTCACAGATGATTAAATGCTATGAT 1075
Qy      364 -----GlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisSerPheMet 380
Db      1076 GTTGGCAAAAGCCCAAGAGTCCCTATTTTCATGCGGAGATGAGGTTATCAATAACTT 1135
Qy      381 TRPAspSerArgLeuPheAsnTyrGlySerTyrGlyValLeuArgPheLeuLeuSerAsn 400
Db      1136 TGGGATAGTCGGCTGTTCACACTATGCTAATGAGGATTAAGGTTCTTCTTCTTAC 1195
Qy      401 AlaArgTyrTrpLeuGlnGlyTyrHisPheAspGlyPheArgPheAspGlyValThrSer 420
Db      1196 CTGAGATATGTTGGATGATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1255
Qy      421 MetMetTyrThrHisSerGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGlyTyrPhe 440
Db      1256 ATGCTGTATCATCATCAGCATGCTACATGATGGGTTTCTGAAATCTACAGAAATATTC 1315
Qy      441 GlyPheAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuHis 460
Db      1316 AGTTTGACACAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1375
Qy      461 GlyLeuHisProAspAlaValSerIleGlyGlnAspValSerGlyMetProThrPheCys 480
Db      1376 AAACCTTTCGCCAAGACAACTGTTGTTGCTGAAAGATTTTCAAGCAGCGCTCTTGC 1435
Qy      481 IleProValProAspGlyGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAsp 500
Db      1436 CGGCGAGTTGAGAAAGTGGCGTGGTGTGATGATGATGATGATGATGATGATGATGAT 1495
Qy      501 LysTyrIleGlnLeuLeuLysGlnSerAspGlnSer---TyrLysMetGlyAspIleVal 519
Db      1496 AGATGATTTGACATCCTGAAATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1555
Qy      520 HisThrLeuThrAsnArgArgTyrPheGlnGlyCysValThrTyrAlaGlnUserHisAsp 539
Db      1556 CATACTTTCATACAGAGATATCTGAAATAATGATCGCATGCTGAGAGCCATGAT 1615
Qy      540 GlnAlaLeuValGlyAspLysThrIleAlaPheThrPheMetAspLysAspMetTyrAsp 559
Db      1616 CAGTCATTTGTTGGCACAATAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1675
Qy      560 PheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLys 579
Db      1676 GGCATGTTCAGACTTCAGCTCTTCACTTCAATATGATGAGGATGATGATGATGATGATGAT 1735
Qy      580 MetIleArgLeuValThrMetGlyLeuGlyGlyGlnGlyTyrLeuAsnPheMetGlyAsn 599
Db      1736 ATGATTCATCTTCACTCAATAGGCCCTTGGAGGTGATGCTACTTGAATTTATGGGAAAT 1795
Qy      600 GlnPheGlyHisProGlnTyrIleAspPheProArgGlyProGlnThrLeuProThrGly 619
Db      1796 GAGTTTGGTCAACCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1851
Qy      620 LysValLeuProGlyLysAsnAsnSerTyrAspLysCysArgArgPheAspLeuGly 639

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Db      1832 -----GAAGGAAACACTGAGCTATGATTAATGACAGACAGTGGAGCTTGTG 1882
Qy      640 AspAlaAspPheLeuArgTyrHisGlyMetGlnGlyPheAspGlnAlaMetGlnHisLeu 659
Db      1883 GACACTGATCACTTGGCGGTACAAATGATCAATGATGATGATGATGATGATGATGATGATGAT 1942
Qy      660 GlnGlnLysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGlnGln 679
Db      1943 GATGAGAGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2002
Qy      680 AspLysValIleIlePheGlnArgGlyAspLeuValPheValPheAsnPheHisTyrSer 699
Db      2003 GAAAAGGTTATTTCTTGTGAAAGTGAAGATTAATTTGTTTCAATTTCCATCCCAAG 2062
Qy      700 AsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeu 719
Db      2063 AAACTTTCAGAGGCTTACAAATGGATGCGATTTGCTTGGGAAATACAGATAGCCCTG 2122
Qy      720 AspSerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPhe 739
Db      2123 GACTGTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2182
Qy      740 ThrThr-----GlnHisProHisAspAsnArgProArgSer 751
Db      2183 ACGTGCCTGAAGGGGTGCGCAGGGGTGCCCGAAACGAACCTTCAACAACCGCGCAACTCG 2242
Qy      752 PheSerValTyrThrProSerArgThrAlaValTyr 764
Db      2243 TTCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2281

RESULT 14
US-09-257-894-19/c
Sequence 19, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Brogile, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2467 base pairs

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STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-09-257-894-19

Alignment Scores:

Pred. No.: 1.54e-229 Length: 2487
 Score: 2146.00 Matches: 395
 Percent Similarity: 71.57% Conservative: 101
 Best Local Similarity: 57.00% Mismatches: 171
 Query Match: 51.48% Indels: 26
 Gaps: 6

US-09-508-377-12 (1-768) x US-09-257-894-19 (1-2487)

QY AspGlyGlnuysileTYrGluileaspProthrleuysaspPheargserhisleuasp 105
 Db GACATCTCCCAATATAGCACTGAGCCCAAGCTGAGATATTCAGAGCATTTCAAG 2077
 QY TyrArgTyserGluTYrArgArgileargalaalaleaspGlnhisgluileu 125
 Db TACCGGATGAAAGAGTCTTAGAGCAGAAAGGATCAATTGAAATGAGGAAATCTT 2017
 QY GluAlaPheSerArglyTYrGluuylseuGlyPheThrArgSerAlaGluGlyleThr 145
 Db GAATCTTTTCTAAAGCTATTGAAATTTGGATTTATACAAATGAGAGTGAAGTGA 1957
 QY TyrArgGluTPAlaProGlyAlaHisSerAlaAlaLeuValGlyAspPheasnentp 165
 Db TATGTGTAATGGCACTGCTGCGCAGAGGAGGAGCTTATTGTGACTTCATGACTGG 1897
 QY AsnProasnAlaaspThmetThrArgaspArgTYrGlyValTPGluilePheleuPro 185
 Db AATGTCGCAACCAATAGATGAGAAAGATTAATTGGTGTGGTCGATCAAAATTT--- 1840
 QY AsnAsnAlaaspGlySerProAlaileProHISGlySerArgValIleArgMetasp 205
 Db GACCATGTCAAGGAGAACTGCTCAATCTCTCAATTCAGAGTTAAATTCGCTTTCA 1780
 QY ThrProserGlyValIleaspSerIleSerAlaTPRileaspPheSerValGlnAlaPro 225
 Db CATGTGAGATATGGGTTGATCGTATTCAGCATTTATTCGTTATGCACTGTGATGCC 1720
 QY GlyGluile-----ProPheasnGlyleTYrTYrAspProGluGluGluuylseTYr 243
 Db TCTAAATTTGAGCTCCCATGATGATGTTCAATGGGATCTCTCTCTCTGTAAGGATAC 1660
 QY ValPheGlnHisProGluProGlyAspProGluSerleuArgileTYrGluSerHisile 263
 Db ACATTTAAGCATCTGCGCTTCAAAGCTGCTGCTCCACGATCTCTATGAGGCCATGTA 1600
 QY GlyMetSerSerProGluProGlyAsnSerTYrAlaAsnPheArgaspGluValleu 283
 Db GGTATGAGTGGTGAAGAACGACAGATAGACATATAGGGAATTTGACAGCATATGTTG 1540
 QY ProArgIleuArgleuGlyTYrAsnAlaValGlnIleMetAlaileGlnGlnHisSer 303
 Db CCACCATATCGAGCAATTAACACACACAGTTCAGTTGATGAGCATTTAGAGCATTCG 1480
 QY TyrTYrAlaSerPheGlyTYrHisValThrAsnPhePheAlaProserSerArgPheGly 323
 Db TACTATGCTTTCTTCCGATACATGTGACAAATTTCTTCCGCTAGCAGACATCTAGCC 1420
 QY ThrProGluAspLeuysSerleuileaspArgAlaHisgluileuGlyleuLeuValleu 343
 Db AACCCAGAGACCTCAATATCTTGTGATTAAGGACACAGTTTGGGTTTCCGAGTTCTG 1360
 QY MetAspIleValHisSerHisSerSerAsnAsnThrleuAspGlyleuAsnGlyPheAsp 363
 Db ATGGATGTTGTCATGCGATGCAAGTAAATATGTCACAGATGTTTAAATGGCTATGAT 1300
 QY GlyThrAspThrHisTYrPheHisgluileProArgGlyHisIleStrpMet 380
 Db -----GlyThrAspThrHisTYrPheHisgluileProArgGlyHisIleStrpMet 380

Db GTTGGACAAAGACCCCAAGATCTCTATTTTCATGCGGAGATAGAGTTATCATMACTT 1240
 QY TrpAspSerArgleuPheAsnTYrGlySerTYrGluValleuArgPheleuSerAsn 400
 Db TGGGATATGCTGGCTGTTCACATATGCTACTGAGAGTATTAAGTTCTTCTTTCTTAC 1180
 QY AlaArgTrpTPleuGluGluTYrLysPheAspGlyPheArgPheaspGlyValHisSer 420
 Db CTGAGATATTTGGTTGATGATTAATTCATGTTGATGCTCCGATTTGATGAGTTACATCA 1120
 QY MetMetTYrThrHisHisgluileuGlnMetThrPheThrGlyAsnTYrGlyGluTYrPhe 440
 Db ATGCTGTATCATCATCATGATGATCAATGAGGTTTACTGAACTACAGAAATATTTTC 1060
 QY GlyPheAlaThrAspValaAspAlaValaTYrleuMetleuValaAsnAspLeuIleHis 460
 Db AGTTTGACACACCTGATGATGAGTGTGTTTACATGATGCTTGCAAACCATTTATATGAC 1000
 QY GlyLeuHisProAspAlaValSerIleGlyLysAspValSerGlyMetProThrPheCys 480
 Db AAATCTCTGACAAAGCACTGTTGTTGCTGAGATGTTTCAGGCAATGCCGCTCTTGC 940
 QY IleProValProaspGlyGlyValGlyPheaspTYrArgleuHisMetAlaValaAsp 500
 Db CGGCCAGTTGATGAGAGTGGGTTGGTTGACTATGCTGCAATGCGCAATGCTATCTGAT 880
 QY LysTPRileGluileuLeuLysGlnSerAspGluSer---TPRlyMetGlyAspIleVal 519
 Db AGATGATGATACCTCACTGAAAGATTAAGATGACTCTGATGCTGATGCTGAAATACG 820
 QY HisThrleuThrAsnArgArgTrpLeuGluLysCysValThrTYrAlaGluSerHisasp 539
 Db CATACCTTGACTAACAGAGATATACGAAATAATGATCGCATATGCTGAGAGCCATGAT 760
 QY GlnAlaLeuValGlyAspIleSThrIleAlaPheTrpLeuMetAspLysAspMetLysasp 559
 Db CAGTCTATTTGTCGCGCAAAACATATGCAATTTCTCCGATGAGCAAGAAATGTAACCT 700
 QY PheMetAlaLeuAspArgProserThrProArgIleAspArgIleAlaLeuHisLys 579
 Db GGCTGTGACACCTTGCCGCTCTTCACTTCAATTTATCAGAGATTCGACTCCAAAG 640
 QY MetIleArgleuValThrMetGlyLeuGlyGlyGluTYrleuAsnPheMetLysasn 599
 Db ATGATTCACCTTCATCAACATGCGCTTGAGAGTATGCTCAATTTATGAGGAAT 580
 QY GluPheGlyHisProGluTPRileaspPheArgArgGlyProGlnThrleuProthrGly 619
 Db GAGTTTGTCACCCAGATGATGATTCATTCAGAA----- 544
 QY LysValleuProGlyAsnAsnAsnSerTYrAspLysCysArgArgPheaspLeuGly 639
 Db -----GAGGAGAACACTGAGCTATATATTAATCAAGACAGACAGCTTGAG 493
 QY AspAlaaspPheleuArgTYrHisgluileGlnGluPheaspGlnAlaMetGlnHisleu 659
 Db GACACTGATACCTTGCGGTTAACAATGATGATGAGTTTACCAAGCATGATGCGCTC 433
 QY GluGluLysTYrGlyPheMetThrSerGluHisgluTYrValSerArgLysHisgluGlu 679
 Db GATGAGAGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 373
 QY AspLysValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisStrpSer 699
 Db GAAABGGTTATTTGCTTTGAAACGTGAGATTTAGTTTGTGTTTCAATTTCCATCCAG 313
 QY AsnSerPhePheaspTYrArgValGlyCysSerArgProGlyLysTYrValaAlaLeu 719
 Db AAAACTTAACGAGGCTACAAAGTGGAGTGCATTTGCTGGGAAATATACAGATAGCCCTG 253
 QY AspSerAspAspAlaLeuPheGlyGlyPheSerArgleuAspHisAspValaAspTYrPhe 739
 Db GACTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 193
 Db -----GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 193

QY 740 ThrThr-----GluHisProHisAspAsnArgProArgSer 751
Db 192 ACCTCCCTCGAAGGGGTGCAGGGGTGCCGAAACGAACCTTCAACACCGCGCCGAACCTCG 133
QY 752 PheSerValTyrThrProSerArgThrAlaValValTyr 764
Db 132 TTCAAAGTCCTTCTCCGCCCCGACCTGTGTGCTTAT 94

RESULT 15
US-09-257-894-24
Sequence 24, Application US/09257894
Patent No. 6376749

GENERAL INFORMATION:
APPLICANT: Biogile, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ. ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-257-894-24

Alignment Scores:
Pred. No.: 1,62e-229 Length: 2565
Score: 2146.00 Matches: 395
Percent Similarity: 71.57% Conservative: 101
Best Local Similarity: 57.00% Mismatches: 171
Query Match: 51.48% Indels: 26
DB: 4 Gaps: 6

US-09-508-377-12 (1-768) x US-09-257-894-24 (1-2565)

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QY 106 TyrArgTyrSerGluTyrArgArgIleArgAlaIleAspGlnHisGluGlyLeu 125

301 TACCGATGAAAAAGATTCCTAGACGAGAAAGATCAATTGAAAGAAAATGAGGAGCTT 360
QY 126 GluAlaPheSerArgGlyTyrGluIleLeuGlyPheThrArgSerAlaGluGlyIleThr 145
Db 361 GAATCTTTTCTAAAGGCTATTTGAAATTTGGGATTAATCAATATGAGATGGAACGTGA 420
QY 146 TyrArgGluTyrAlaProGlyAlaHisSerAlaIleValAlaGlyAspPheAsnThr 165
Db 421 TATCGTAATGGGACCTCTGCGGAGAGGACAGCTTATGAGTGCCTTCAATGATCGG 480
QY 166 AsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTyrGluIlePheLeuPro 185
Db 481 AATGGTGCAACCATTAAGATGAGAAAGATTAATTTGGTGTGGTGCATCAAAATTT--- 537
QY 186 AsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAsp 205
Db 538 GACCATGTCAAAGGAGAAACCTCCATCCCTCAATCCAAATTCAGGTTAAATTCGCTTCTA 597
QY 206 ThrProSerGlyValLysAspSerIleSerAlaTyrIleLysPheSerValGlnAlaPro 225
Db 598 CATGCTGAGATGGGTTATGCTATTCAGCATTAATTCGTTATGAGGACTGTGATGCC 657
QY 226 GlyGluIle-----ProPheAsnGlyIleTyrTyrAspProProGluGluGluTyr 243
Db 658 TCTAATTTGGAGCTCCCTATGATGATGCTGATGAGTGTGATGCTGCTGCTGTAAGGTAC 717
QY 244 ValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrGluSerHisIle 263
Db 718 ACATTAAAGCATCTCGGCTTCAAAAGCTGCTCCACGTATCTATGATGAGCCCATGTA 777
QY 264 GlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGluValIle 283
Db 778 GGTATGATGTTGAAAAAGCCAGCAGTACACATTAAGGAATTTGACAGCATGTGTTG 837
QY 284 ProArgIleLeuArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGluHisSer 303
Db 838 CCAGCATACGAGCAAAATTAATACACACAGATTCAGTTGATGAGCATTAAGGACATTCG 897
QY 304 TyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGly 323
Db 898 TACTATGCTCTTTCGGGTACCATGACAAATTTCTTGGCGTTGACACAGATTCAGGC 957
QY 324 ThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeuValIle 343
Db 958 ACACCAAGAGACCTCAATATCTTGTATTAAGCACAAGTTGGGTTGCCAGTTCTG 1017
QY 344 MetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAsp 363
Db 1018 ATGATGTTGTCATATAGCATCAAGTAAATATGCAAGATGTTTAAATGGCTATGAT 1077
QY 364 -----GlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisHisIleTyrMet 380
Db 1078 GTTGACAAAGCACCCAAAGATCTTATTCAGCGGAGATAGAGATATCAATAACTT 1137
QY 381 ThrAspSerArgLeuPheAsnTyrGlySerTyrGluValLeuArgPheLeuSerAsn 400
Db 1138 TGGATATGTCGCTGTTCAACTATGCTACTGAGAGATATTAAGTTCTTCTTTCTTAC 1197
QY 401 AlaArgTyrIlePheGluGluTyrIlePheAspGlyPheArgPheAspGlyValThrSer 420
Db 1198 CTGAATATATTTGGTATGATATCAATGATTTGATGAGTTGATGAGATTAATCA 1257
QY 421 MetMetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGluTyrPhe 440
Db 1258 ATGCTGATCATCACATGATGATCAATGTGGGTTACTGGAACCTACAGGATATTTTC 1317
QY 441 GlyPheAlaThrAspValAspAlaValIleTyrLeuMetLeuValAsnAspLeuIleHis 460
Db 1318 AGTTTGACACACGCTGTGATGCAATGTTTACATGATGCTTCCAAACCATTAATGAC 1377
QY 461 GlyLeuHisProAspAlaValSerIleGlyAspValSerGlyMetProThrPheCys 480
Db 1378 AAACCTTGCCAGAGCAACTGTTGCTGAAGATGTTTCAAGGATGCGCGTCTTTC 1437


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QY 481 IleProValProAspGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAsp 500
Db 1438 CGGCCAGTTGATGAAGGTGGGGTTGGGTTGACTATCGCCTGGCAATGGCTATCCCTGAT 1497
QY 501 LysTrpIleGlyLeuLeuLeuGlnSerAspGluSer---TrpLysMetGlyAspIleVal 519
Db 1498 AGATGGATTGACTACCTTAAGATTAAGATGACTCGACTGGTTCGATGGTGTAATATAGCG 1557
QY 520 HistTrpLeuTrpAsnArgArgTrpLeuGlyLysCysValThrTyrAlaGluSerHisAsp 539
Db 1558 CATACTTGCATCAACAGAGATATCTGAAATATGCATCGCATATGCTAGAGCCATGAT 1617
QY 540 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 559
Db 1618 CAGTCTATTGTTGGCAGCAAACTATTGCATTCTCTGATGACACAGGAAATGTACACT 1677
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Db 1678 GGCATGTCAGACTTCAGCTGCTTCCTACCTACATTTGATCGAGGATTCACCTCCAAAG 1737
QY 580 MetIleArgLeuValThrMetGlyLeuGlyGlyGlyGlyTyrLeuAsnPheMetGlyAsn 599
Db 1738 ATGATTCATCTTATCAACATGGCCCTTGGAGGTGATGGCTACTTGAATTTATGGGAAT 1797
QY 600 GluPheGlyHisProGluTrpIleAspPheProArgGlyProGlnThrLeuProThrGly 619
Db 1798 GAGTTTGGTCACTCCAGAAATGATGACTTCCAGA----- 1833
QY 620 LysValLeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgAspPheAspLeuGly 639
Db 1834 -----GAAAGGAACAATGAGCTATGATTAATTAACAGACAGACAGAGCTTGTG 1884
QY 640 AspAlaAspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeu 659
Db 1885 GACACTGATCACTTCGCGTACAGATACATGATGCGTTGACCAAGCATGATGCGCTC 1944
QY 660 GluGluLysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGluGlu 679
Db 1945 GATGAGAGATTTCTTCTTCCTTCCTTCGTCGTAAGCAGATGCTCAGCATGAACGATGAG 2004
QY 680 AspLysValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTrpSer 699
Db 2005 GAAAGGTTATGCTTTGAAAGTGAGATTTAGTTTGTTCATTTCCATCCCAAG 2064
QY 700 AsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLysTyrIleValAlaLeu 719
Db 2065 AAAACTTACAGAGGCGCTACAAAGTCGATCGATTTGCCCTGGGAAATACAGAGTAGCCCTG 2124
QY 720 AspSerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPhe 739
Db 2125 GACTCTGATGCTCTGCTTCCTTCGTTGAGATGAGATGAGCCACGACGTGATCACTTC 2184
QY 740 ThrThr-----GluHisProHisAspAsnArgProArgSer 751
Db 2185 ACGTGCCTGAAGGGGTGCGAGGGGTGCCCGAAACGAACTTCAACAAACGGCCGAACCTCG 2244
QY 752 PheSerValTyrThrProSerArgThrAlaValValTyr 764
Db 2245 TTCAAAGTCTTCTTCGCGCCGCACTGTGTGCTTAT 2283
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Search completed: April 17, 2004, 22:37:41
Job time : 180 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_pzn model

Run on: April 17, 2004, 18:29:50 ; Search time 540 Seconds
(without alignments)

6041.882 Million cell updates/sec

Title: US-09-508-377-12

Sequence: 1 MATFAVSGATLGVARRPPAAA.....PRSFVYTPERTAVVATL 768

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Egapop 6.0 , Egapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ pzn.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09508377/runat.15042004.084305.2294/app.query.fasta_1.967
-DB=N Geneseg 23Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdd
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09508377@cgn.1.1.352@runat.15042004.084305.2294 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
N_Geneseg_29Jan04:*
1: genesegn1908:*
2: genesegn1908:*
3: genesegn2000:*
4: genesegn2001as:*
5: genesegn2001bs:*
6: genesegn2002as:*
7: genesegn2003as:*
8: genesegn2003bs:*
9: genesegn2003cs:*
10: genesegn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4169	100.0	2726	5	AAH78337
2	3685	88.4	3015	2	AAV05639
3	3363	80.7	3039	6	ABK15494
4	3362	80.6	2919	2	AAQ73750
5	3352	80.4	2968	5	AAH78342
6	3351	80.4	2640	2	AAV70961
7	3342	80.2	2725	2	AAV29757
8	3341	80.1	2665	2	AAV69729

9	3337.5	80.1	2655	7	ADA71289	Ada71289	Rice	gene
10	3292	79.0	3090	2	AAV38720	AAV38720	Full	leng
11	3258	78.1	2418	6	AB213067	AB213067	Arabidops	
12	3258	78.1	2418	7	ADA68438	ADA68438	Arabidops	
13	3241.5	77.8	2913	2	AAV38719	AAV38719	Full	leng
14	3197	76.7	2531	2	AAV17267	AAV17267	Class A s	
15	3197	76.7	2563	5	ABK50301	ABK50301	Potato	cd
16	3193	76.6	3074	2	AAV69587	AAV69587	Potato	st
17	3189	76.5	2529	2	AAV42637	AAV42637	Class A s	
18	3189	76.5	2507	2	AAV42631	AAV42631	Class A s	
19	3164.5	75.9	2307	9	ADC07807	ADC07807	Rice	DNA
20	3164	75.9	3231	6	AAV42632	AAV42632	Class A s	
21	3155	75.7	2577	6	AB212532	AB212532	Arabidops	
22	3155	75.7	2715	3	AAV45939	AAV45939	Arabidops	
23	3152.5	75.6	2576	2	AAV42636	AAV42636	Class A s	
24	3152	75.6	3003	2	AAV42634	AAV42634	Class A s	
25	3135	75.2	3033	2	AAV42630	AAV42630	Class A s	
26	3133	75.1	2975	2	AAV42635	AAV42635	Class A s	
27	3082.5	73.9	2304	9	ADC08218	ADC08218	Rice	DNA
28	2824	70.1	2087	2	AAV69737	AAV69737	Corn	star
29	2917	70.0	2165	2	AAV69736	AAV69736	Corn	star
30	2900	69.6	2307	3	AAV29938	AAV29938	DNA	encod
31	2336.5	56.0	11475	5	AAV78338	AAV78338	Nucleotid	
32	2301	55.2	11473	2	AAV34650	AAV34650	starch	br
33	2233	53.6	1919	2	AAV38722	AAV38722	Corn	star
34	2196	52.7	4563	4	AAV30910	AAV30910	Wheat	sta
35	2166.5	52.0	2733	3	AAV62135	AAV62135	Rice	star
36	2163.5	51.9	3128	2	AAV00774	AAV00774	Potato	st
37	2157.5	51.8	2733	2	AAV54674	AAV54674	Rice	star
38	2155	51.7	2289	7	AAV71346	AAV71346	Rice	gene
39	2155	51.7	2289	9	ADC08304	ADC08304	Rice	DNA
40	2146	51.5	2487	2	AAV69747	AAV69747	Corn	star
41	2146	51.5	2565	2	AAV69752	AAV69752	Corn	star
42	2146	51.5	2763	2	AAV29758	AAV29758	zea	mays
43	2146	51.5	2771	2	AAV24257	AAV24257	Branching	
44	2146	51.5	2772	2	AAV69740	AAV69740	plasmid	p
45	2140	51.3	2899	4	AAV02926	AAV02926	Human	she

ALIGNMENTS

RESULT 1
AAH78337
ID AAH78337 standard; cDNA; 2726 BP.

26-NOV-2001 (first entry)

Nucleotide sequence of wheat starch branching enzyme 9 (BEIIa).

Wheat; starch branching enzyme; BEIIa; BEIID; SBE; transgenic plant; starch biosynthetic pathway; amylopectin; amylose; ss.

Triticum sp.

WO200162934-A1.

30-AUG-2001.

21-FEB-2001; 2001WO-AU000175.

21-FEB-2000; 2000AU-00005742.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

(GOOD-) GOODMAN FIELDER LTD.

(LIMA-) GRP LIMABRAIN PACIFIC PTY LTD.

Morell M, Rahman S;

WPI; 2001-570635/64.

altering the amylose and amylopectin content of cereal plants, e.g. wheat and barley.

Example 1; Fig 1; 103bp; English.

The present sequence encodes wheat starch branching enzyme 9, designated CC BR1a. The specification describes BE1b. BE1b is a type II starch branching enzyme (SBE). The BE1b nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant

Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2726
Score: 4169.00 Matches: 768
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-508-377-12 (1-768) x AAH76337 (1-2726)

QY 1 MetLathrPheAlaValSerGlyAlaThrLeuGlyValAlaArgProProAlaAla 20
DB 124 ATGGCGAGGTTGCGGGTCCGCGCGGACCCCTCGGTGTGGCGGGCGCGCGCGGCG 183
QY 21 GluProGluGluLeuGlnIleProGluAspIleGluGluGlnThrAlaGluValAsnMet 40
DB 184 CAACCTGAAGATTACAGATACCTGAAGACATCGAGGACCAACGGCTGAAGTAAACATG 243
QY 41 ThrGlyThrAlaGluLeuGluSerSerGluProThrGlnGlyIleValGluThr 60
DB 244 ACAAGGGGGAGCTGCAGAAAACTGAAATCTCAGAAACCACTCAAGGCATTGGGAAACA 303
QY 61 IleThrAspGlyValThrLeuGlyValIleGluValValGluValProAspVal 80
DB 304 ATCACTGATGGTGACCAAGAGAGTTAAGGACTAGTGTGGGGAGAAACCGCAAGTT 363
QY 81 ValProLysProGlyAspGlyGlnLysIleTyrgLulleAspProThrLeuAspPhe 100
DB 364 GTCCCAAAACCAAGAGATGGGCGAAGAAATACGAGATTGACCCAAACGCTGAAGATTTT 423
QY 101 ArgSerHisLeuAspTyraGlyTyserGlyTyraGlyIleArgAlaAlaIleAspGln 120
DB 424 CGAGGACCATCTTGACTACCGATACAGCGAATACAGAGAAATCTGCTCTATTGACCA 483
QY 121 HisGluGlyValLeuGluAlaPheSerArgGlyTyrgLulleAspGlyPheThrArgSer 140
DB 484 CATGAAGGTGGATTGGAAGCATTTTCTCGGTATGAAAGCTTGGAATTTACCCCAAGT 543
QY 141 AlaGluGlyIleThrTyraGlyLulleAspGlyAlaHisSerAlaIleValAlaValGly 160
DB 544 GCTGAAGGTATACCTTACCGAAGATGGGCTCTCGAGGCGCATTTCTCAGATTAAGAGT 603
QY 161 AspPheAsnAspTyrAsnProAsnAlaAspThrMetThrArgAspAspTyrglyValTyr 180
DB 604 GACTTCAACAATTGGAATCCGATGAGTACTATACACAGATATTAATGATGATTTGG 663
QY 181 GluIlePheLeuProAsnAspAlaAspGlySerProAlaIleProHisGlySerArgVal 200
DB 664 GAGATTTTCTCCCTCAACATGATGATGATCCCGACGCTATTTCTCAGCTCAGCTGAT 723
QY 201 LysIleArgMetAspThrProSerGlyValLysAspSerIleSerAlaTyrIleTyrsPhe 220
DB 724 AAGATACCGATGGATCTCATCTGTGTGAAGATTCAATTTCTGCTTGATCAAGTTTC 783
QY 221 SerValGlnAlaProGlyGluIleProPheAsnGlyIleTyrgTyrsProProGluGlu 240
DB 784 TCTGTGACGGCTCCAGGTGAATATCAATCAATGAGGATATATTATATGATCACTGAAGAG 843

QY 241 GluTyraValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrgL 260
DB 844 GAGAGTATGTTCTCCACATCTCAACCTAAACCAAGATCACTGAGGATTTATGAA 903
QY 261 SerHisIleGlyMetSerSerProGluProLysIleAsnSerTyraAsnPheArgAsp 280
DB 904 TCACACATGGATGATGACGAGCCAGAACCGMAATTAATTCATATGCTAATTTAGGAT 963
QY 281 GluValLeuProArgIleLysArgLeuGlyTyraAsnAlaValGlnIleMetAlaIleGln 300
DB 964 GAGGTCTCCAGAAATTAAAGGCTTGATTAACATGCACTGCAGTAATAGCAATCCAG 1023
QY 301 GluHisSerTyrgTyraSerPheGlyTyraHisValThrAsnPheAlaProSerSer 320
DB 1024 GAGCATTTCAATATGCGAGCTTTGGGTACATGTTACTATTTTGGACCAAGTAC 1083
QY 321 ArgPheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeu 340
DB 1084 CGTTTGGAACTCCAGAGGACTTAAATCCCTGATCATGAGACATGAGACTTGGATTG 1143
QY 341 LeuValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsn 360
DB 1144 CTGTGTTATGAGATTTGTTCTCATGTCATTCATCAATATATACCTTGACGCTGAT 1203
QY 361 GlyPheAspGlyThrAspThrHisTyraPheHisGlyGlyProArgGlyHisIleTyrPhe 380
DB 1204 GGTTCGATGAGCATGATACCATTTACTTCCACGGTGTGTCCAGCTGGCCATCATGATG 1263
QY 381 TyrAspSerArgLeuPheAsnTyrglySerTyrGluValLeuArgPheLeuLeuSerAsn 400
DB 1264 TGGGATTTCTGCTATTCACATGAGAGTGGAGATGGAATGAAATCTTCTGCAAC 1323
QY 401 AlaArgTyrTrpLeuGluGluTyrgTyraPheAspGlyPheArgPheAspGlyValThrSer 420
DB 1324 GCGAGATGGTGGCTTGAAAGATTAATGATTGATGATTTGATTTGATGGGGTGCTCC 1383
QY 421 MetMetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrglyGluTyraPhe 440
DB 1384 ATGATGATATCTCAACCATGATTCATCAATGCAATTTACTGGGAATATGCGAGATATTT 1443
QY 441 GlyPheAlaThrAspValAspAlaValAlaTyrgLeuMetLeuValAsnAspLeuIleHis 460
DB 1444 GGAATTCATCTGATGTGATGCGGTGATTACTGTGATGCTGCAAGATCTAATTCAT 1503
QY 461 GlyLeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCys 480
DB 1504 GSACTTCATCTGATGCTGTATTCATTTGGTGAAGATGCAATGCCACATTTGGC 1563
QY 481 IleProValProAspGlyGlyValGlyPheAspTyraGluHisMetAlaValAlaAsp 500
DB 1564 ATCCCGTTCCAGATGTGTGGTGTGTTTACATGCTGATGCTGATGCTGATGACAGAT 1623
QY 501 LysTyrIleGlyLeuLeuLysGlnSerAspGlySerTyrPheMetGlyAspIleValHis 520
DB 1624 AAATGATTAACCTCCAGCAAGGACCAATCTTGAAAGAGGGGTGATATTTGGC 1683
QY 521 ThrLeuThrAsnArgTyrTrpLeuGlyLysCysValThrTyraGluSerHisAspGln 540
DB 1684 ACCCTTAACAATAGAGAGTGGCTTGAGAGTGTATCTTATGCAAGAAAGCATGATCA 1743
QY 541 AlaLeuValGlyAspLysThrIleAlaPheTyrLeuMetAspLysAspMetTyraPhe 560
DB 1744 GCACTAGTGGTGAACAAGACTATGCAATTCGTTGATGATGATAGAGATATGATATTC 1803
QY 561 MetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisTyrsMet 580
DB 1804 ATGGCTTGATAGGCTTCAACTCTCGCATTTGATCTGGCATAGCACTTACATATAATG 1863
QY 581 IleArgLeuValThrMetGlyLeuGlyGlyGlyTyrgLeuAsnPheMetGlyAsnGlu 600
DB 1864 ATCAAGCTTGTACCAAGAGGTTTAGGGGTGAAGGCTATCTTAATTCATGGGAATGAG 1923
QY 601 PheGlyHisProGluTyrTrpIleAspPheProArgGlyProGlnThrLeuProThrGlyLys 620

Db	1924	TTTGGGACCTCTGATGGATGATTTTTCGAAAGAGGTCCGCAACTCTTCCACCGGCAA	1983
Qy	621	ValLeuProGlyAsnAsnAsnSer-TyrAspLysCysArgAlaGlnPheAsnLeuGlyAsp	640
Db	1984	GTCTCCCTCGAAATAACAATAGTATGATTAATGCCGCCCTAGATTGATCTTGGAGAT	2043
Qy	641	AlaAspPheLeuArgTyrHisIsgLysMetGlnIuPheAspGlnAlaMetGlnHisLeuGlu	660
Db	2044	GCAATATTTCTTAATATCATGATGATGCAAGATTGCATCGCGCATGCAACATCTTGGAG	2103
Qy	661	GluLysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGluGluAsp	680
Db	2104	GAATAAATATGGGTTTATGACATCTGAGCACCAAGTATGTTTCAACGAAACATGAGGAAGAT	2163
Qy	681	LysValIleIlePheGlnArgGlyAspLeuValPheValPheAsnPheHisTyrSerAsn	700
Db	2164	AAGGTGATCATCTTCGAAAGAGGAGATTGGTATTTGTTTTCACCTTCACCTCGAGCAT	2223
Qy	701	SerPhePheAspTyrArgValGlnCysSerArgProGlyLysTyrLysValAlaLeuAsp	720
Db	2224	AGCTTTTTCATCTCCGTGTTGGGTGTTCCAGGCTGGGAAGTCACAAAGTGGCTTTAGAC	2283
Qy	721	SerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThr	740
Db	2284	TCCGACGATGACCTTTTGGTGATTACGACGGCTTGATTCATGATGTGACTACTTACCA	2343
Qy	741	ThrGlnHisProHisAspAsnArgProArgSerPheSerValTyrTrpProSerArgThr	760
Db	2344	ACCCAAATCATCGCATGACAAACAGGCCGGCTCTTTCGTGGTGTACATCCGACGAGAACT	2403
Qy	761	AlaValValTyrAlaLeuThrGlu	768
Db	2404	GCGGTGCGTATGCGCTTACAGAG	2427

Result 2	AAV05639	AAV05639 standard; cDNA to mRNA; 3015 bp.
ID	AAV05639	
XX	AAV05639;	
XX		
DT	25-MAR-2003	(revised)
DT	01-MAY-1998	(first entry)
XX		
DE	Rice type IV starch branching enzyme cDNA.	
XX		
KM	Rice; type IV starch branching enzyme; amylopectin synthesis; ds.	
XX		
OS	Oryza sativa.	
XX		
XX	Key	Location/Qualifiers
FH	CDS	129..2654
FT		/*tag= a
FT	sig_peptide	129..287
FT		/*tag= b
FT	mat_peptide	288..2651
FT		/*tag= c
FT		/product= "type_IV_starch_branching_enzyme"
XX		
PN	JP10004970-A.	
XX		
PD	13-JAN-1998.	
XX		
PP	24-JUN-1996;	96JP-00162983.
XX		
PR	24-JUN-1996;	96JP-00162983.
XX		
PA	(MITS-) MITSUI GWOSAI SHOKUBUNSU BIO KENKYUSHO.	
XX	(MITK) MITSUI TOATSU CHEM INC.	
XX		
WR	WPI; 1998-133625/13.	

PT Rice starch branching enzyme gene - synthesises amylopectin to yield high
PT quality starch.

PS Claim 4; Page 5-8; 13pp; Japanese.

CC The present sequence encodes the rice type IV starch branching enzyme,

CC which has the ability to synthesize antipodeolisin. The quality of the
CC improved by the use of the protein. (Updated on 25-MAR-2003 to correct
CC field.)

Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 U; 0 Other;

Alignment Scores:

Score:	3685.00	Matches:	683
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Best Local Similarity: 81.31%  Mismatches: 47
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DB:	2	Gaps:	4
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US-09-508-377-12 (1-768) X AAV05639 (1-3015)

QY 1 MetAlaThrPheAlaValSerGlyAlaThrLeuGlyValAlaArgPro----- 16

Db 1.29 ATGGCGTCTCGCGGTGTCCGGCGCGGAGGCTCGGGTCTGCGGGCGGGGCGGGC 18

QY 17 -----Pro1a1a----- 19

Db 1.89 GCGGCGGGGTGCCCCGCGCGCGATCCGGCGGGTGACTTGCCTCTTC 24

QY 19 ----- 19

Db 249 AGGAGGAGGACTCTCTCACTGCGCTGTGAGCTGCGCGGTCTCTCGGAAGTG 30

Qy 19 ----- 19

Db 309 CTGGTGCCCTGGCGGTGGAGCGACTTGTCTGTCTCCTCTGCGGAACCGAGCGTGAACT 360

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QY      20  --AlaGlnProGluGluLeuGlnIleProGluAsp-----IleGluGlu 33
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Db 369 CAAGAGCAACTGAGAATCTCAGATACCTGATGATAATAAGTAAACCTTTTGAGGAG 42

34 Gln-----ThrAlaGluValAsnMetThrGlyGlyThrAlaGluLysLeu 48

Db 429 GAGGAGAGATTCCAGCAGTGGCAGGACAGCATTAAGGTTGTGGCTGAAGACAAACTT 488

49 GluSerSerGluProThrGlnGlyIleValGluThrIleThrAspGlyValThrLysGly 66

Db 489 GAATCTCAGAAGTGATCAAGACATTGAGGAAATGTGACTGAGGGTGTGATCAAAGAT 544

69 ValLysGluLeuValValGlyGlyLysProArgValValProLysProGlyAspGlyGln 86

Db 549 GCTGATGAACCAACTGTGGAGGATAAACCAAGAGTTATCCCAACCAACGAGATGGGCAG 60

89 LysileTyrgluLeasprrothLeullysAsppheargserhisLeuAsptyrArgtyr 100

Db 609 AAGATATACCAATTGACCCAATGCTGGAAGATTTCGGAACCATCTTGACTACCGATAC 60

109 SerGIuTyrArgargiIeArgAlaAlaIleaspGlnHisGluGlyGlyLeuGluAlaPhe 14

Db 669 AGTGAATACAGAGAATGCGTGACGCTATTGACCAACATGAAGGTGGCTTGGATGCAWTF 74

129 SerArgGlyTyrGluLysLeuGlyPheThrArgSerAlaGluGlyIleThrIleArgGlu 14

Dd 729 TCTCGTGGTTACGAAGCTTGGATTCACCCCGAGCGCTGAAGGCATTACCTACCGAA /

149 TYPALPROGLYALHISSERAALALEUVALGYASBPNEASHASHITPASHIFOASH 10

789 TGGGCACTTGGAGCAACAGTCTGGAGCATTAGTAGGTGACTTCAACAAATGGATCCAAAT 84

169 AlaSPThrMetThrArgAspSPtyrGlyValTrpGluIlePheLeuProAsnAsnAla 16

QY 189 AspGlySerProAlaIleProHisGlySerArgValIleIleArgMetAspThrProSer 208
 Db 909 GATGATCCCTGCTATTCCTCATGGCTCAGCGTAAAGATTCGATGATACCATCT 968
 QY 209 GlyValIleAspSerIleSerAlaTrpIleLysPheSerValGlnIleProGlyGluIle 228
 Db 969 GCGGAAAGGATTCATTCCTCCTGGATTAAGTTGCTGCAAGCTCCAGGTGAAATA 1028
 QY 229 ProPheAsnGlyIleTyrTyrAspProProGluGluGluTyrValPheGlnHisPro 248
 Db 1029 CCGTCAACCGTAT 1088
 QY 249 GlnProLysArgProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerPro 268
 Db 1089 CAACCTAAACGACCAAAATTCGCTCGCGATATATGAAATCATATATGAAATGAAATGACCCG 1148
 QY 269 GluProLysIleAsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArg 288
 Db 1149 GAACCGAAGATTAACACATATCTATTTAGGATGAGGTGCTACCAAGAAATTAATAAG 1208
 QY 289 LeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPhe 308
 Db 1209 CTGGGTACATGCTGTACAGATATGCGAATTCAGAGACGCTTATTCGCAAGCTTT 1268
 QY 309 GlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeu 328
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 QY 329 LysSerLeuIleAspArgAlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHis 348
 Db 1329 AAATCTCGATGATTAACCTACAGAGCTGTTCTGTACTTATGATATGATATGTTGCAC 1388
 QY 349 SerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHis 368
 Db 1389 AGCTATGCTCAACATACCTCCTGATGCTTGAATGCTTGAATGCTTGAATGCTTGAAT 1448
 QY 369 TyrPheHisGlyGlyProArgGlyHisIleTyrMetTrpAspSerArgLeuPheAsnTyr 388
 Db 1449 TACTTCAGATGAGCAACAGCGGCTCATCATGATGCGGATCTCGCCCTGTTCACTAT 1508
 QY 389 GlySerTrpGluValLeuArgPheLeuLeuSerAsnAlaArgTrpTrpLeuGluGluTyr 408
 Db 1509 GGGAGTTGGGAAGTTTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1568
 QY 409 LysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyrThrHisIleGlyLeu 428
 Db 1569 AAGTTTGAAGGATTCATTTGATGGGAGTGAACCTCATGATGATGATGATGATGATGAT 1628
 QY 429 GlnMetThrPheThrGlyAsnTyrGlyGlyTyrPheGlyPheAlaThrAspValAspAla 448
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 QY 449 ValValIleTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSer 468
 Db 1689 GAGATTAATCTTGAAGTGTGTAAGCATTAATTAATTAATTAATTAATTAATTAATTAAT 1748
 QY 469 IleGlyGluAspValSerGlyMetProThrPheCysIleProValProAspGlyGlyVal 488
 Db 1749 ATTGGTGAAGATGTCAGCGGAGTCCACACTTTTGAATTCCTGTTCAGATGGTGGTGT 1808
 QY 489 GlyPheAspTyrArgLeuHisMetAlaValAlaAspLysTrpIleGluLeuLeuLysGln 508
 Db 1809 GGTATTGACTATCGTTGCAATATGCTGTACCGCAAAATGAGATCGAACTCCCAAGCAA 1868
 QY 509 SerArgGluSerTrpLysMetGlyAspIleValHisThrLeuThrAsnArgArgTrpLeu 528
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 QY 529 GluLysCysValThrTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIle 548
 Db 1929 GAGAGTGTGTTATGATGAGAAAGTCAACCAAGCACTAGTGTGTGCAAGACTATT 1988

QY 549 AlaPheTrpLeuMetAspLysAspMetTyrAsnPheMetAlaLeuAspArgProSerThr 568
 Db 1989 GCAATTCGTTGAGTGAAGATTAAGATTAATTAATTAATTAATTAATTAATTAATTAAT 2048
 QY 569 ProArgTrpLeuAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeu 588
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 QY 589 GlyIleGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAsp 608
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 QY 609 PheProArgGlyProGluThrLeuProThrGlyLysValLeuProGlyAsnAsnAsnSer 628
 Db 2169 TTCCCAAGAGCGCCGCAAAAGCTTCCAAATGCTCGCTCCCTCCAGAAACAACCTACCT 2228
 QY 629 TyrAspLysCysArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGly 648
 Db 2229 TTGATTAATGCTCGTGAATTTGATGCTTGAATGATGATGATGATGATGATGATGATGAT 2288
 QY 649 MetGlnIlePheAspGlnAlaMetGlnHisLeuGluGluLysTyrGlyPheMetThrSer 668
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 QY 689 AspLeuValPheValPheAsnPheHisTrpSerAsnSerPhePheAspTyrArgValGly 708
 Db 2409 GATTGGATATCGTTCATCTTCCACATGCGATTAATGATTAATGATTAATGATTAATGAT 2468
 QY 709 CysSerArgProGlyLysTyrLysValAlaLeuAspSerAspAspAlaLeuPheGlyGly 728
 Db 2469 TGTTTAAGCCTGGAAGATGACAAAGATGCTGTGACCTCAGACGATGCGCTCTTGTGTGA 2528
 QY 729 PheSerArgLeuAspHisAspValAspTyrPheThrTrpGluHisProHisAspAsnArg 748
 Db 2529 TTCACTGCGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2588
 QY 749 ProArgSerPheSerValTyrThrProSerArgThrAlaValIleTyrAlaLeuThrGlu 768
 Db 2589 CCATGTTCAATCTCGGTGATACACCCCAAGCAAGACCGCGTGTATGACATTAACAGAG 2648
 RESULT 3
 ID ABK15494 standard; cDNA; 3039 BP.
 AC ABK15494;
 XX 08-MAY-2002 (first entry)
 DT
 DE Wheat starch branching enzyme IIb cDNA from clone wdk2c_pk009.j17.
 XX
 KW Wheat; starch branching enzyme; starch synthesis; transgenic plant;
 KW wdk2c_pk009.j17; antibody; gene mapping; expressed sequence tag; EST;
 KW gene; ss.
 XX
 OS Triticum aestivum.
 XX
 FH Key
 FT CDS
 FT
 FT Location/Qualifiers
 FT 3..2570
 FT /*tag= a
 FT /product= "Starch branching enzyme IIb"
 FT /partial
 FT /note= "No start codon shown. The sequence from
 FT nucleotide 481-3039 is specifically claimed in claim 3
 FT of the specification and is shown as Seq ID. 1"
 PD 03-JAN-2002
 US2002002713-A1.

FF 23-FEB-2001; 2001US-00792127.
XX 01-MAR-2000; 2000US-0186098P.
XX (ALLE/) ALLEN S M.
PA (BECK/) BECKLES D M.
PA (BUTL/) BUTLER K H.
XX (PEAR/) PEARLSTEIN R W.
PI Allen SM, Beckles DM, Butler KH, Pearlstein RW;
XX MPI; 2002-179859/23.
DR P-PSDB; A0U76219.
XX
PT Novel isolated polypeptide having starch IIB enzyme activity, useful for
PT preparing antibodies to the proteins which are used to detect the
PT polypeptides in situ in cells or in vitro in cell extracts.
XX
PS Claim 3, Page 17-18; 27pg; English.

XX This invention relates to the cDNA and protein sequences of a novel wheat
CC starch branching enzyme IIB enzyme. Starch branching enzymes are
CC responsible for the formation of alpha 1-6 linkages in amylopectin in the
CC starch synthesis pathway. The nucleotide sequence of the invention is
CC useful for producing a transgenic plant expressing the starch branching
CC enzyme. The protein sequence is useful for preparing antibodies against
CC starch branching enzyme IIB protein, which are useful for detecting the
CC proteins in situ in cells, or in vitro in cell extracts. The protein is
CC also useful for selecting an isolated polynucleotide that affects the
CC level of expression of a starch branching enzyme IIB protein or enzyme
CC activity in a plant cell. All or substantial portion of the nucleotide
CC sequence can be used as probe for genetic and physical mapping of the
CC genes and can be used as markers for traits linked to those genes. This
CC information is useful in plant breeding in order to develop lines with
CC desired phenotypes. A polynucleotide fragment is useful for isolating
CC cDNAs and genes encoding homologous proteins from the same or other plant
CC species. They are also useful as DNA hybridisation probes or as
CC polymerase chain reaction (PCR) amplification primers. The fragments are
CC also useful for creating transgenic plants and may be useful as
CC restriction fragment length polymorphism markers. Nucleic acid probes
CC derived from the cDNA sequence may also be used for physical mapping or
CC for fluorescence in situ hybridisation (FISH) mapping. The present
CC sequence represents the wheat starch branching enzyme IIB cDNA from clone
CC wdk2c.pK009.j17
XX
XX
XX
SQ Sequence 3039 BP; 836 A; 624 C; 783 G; 796 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.57e-309 Length: 3039
Score: 3363.00 Matches: 607
Percent Similarity: 89.27% Conservative: 75
Best Local Similarity: 79.45% Mismatches: 68
Query Match: 80.67% Indels: 14
Gaps: 4

US-09-508-377-12 (1-768) x ABR15494 (1-3039)

QY 7 SerGlyAlaThrLeuGlyValAlaArgProAlaAlaAlaGlnPro----- 22
Db 294 AGTGGCGGAACA-----CCGCTTCCATCGACGCTCCCTTCAGTTGCAT 338
QY 23 ---GluGluLeuGlnIleProGluIleGluGluGlnThrAlaGluValAsnMetThr 41
Db 339 TCTGATGATCTGAAGGTTCCA---TTCATTGATGATGAACA-----AGCTTCAG 386
QY 42 GlyGlyThrAlaGluLeuGluLeuSerGluProThrGlnGlyIleValGluThrIle 61
Db 387 GATGAGGTGAAGATGATGTTGGCTTCAGAGACAAGTCAAGTTAGTGAAGAAATTGAT 446
QY 62 ThrAspGlyValThrIleGlyValIleGluLeuValIleGlyIleGluProAspValVal 81
Db 447 GCTGAAGACGACGAGATGACAAAGATCTCTCAACGAGGAGAAATTACCATTTCTG 506

QY 82 ProLysProGlyAspGlyGlnLysIleTyrGluIleAspProThrLeuLysAspPheArg 101
Db 507 CCACCACCGGGAAATGACACAGCAATATACGAGATTGACCCCAACCTCCGACACTTAAG 566
QY 102 SerHisLeuAspTyrArgTyrSerGluTyrArgArgGlyLeuArgAlaAlaIleAspGlnHis 121
Db 567 TACCACTTGGATTCGATATAGCTTATACAGAGAAATACGTTCCACACATTTGATGAAC 626
QY 122 GluGlyGlyLeuGlnAlaPheSerArgGlyTyrGlyLysLeuGlyPheThrArgSerAla 141
Db 627 GAAGAGGACATGATGATTTTCCCGCGGTTACAGAAAGTTTGATTTAGCGACCGCT 686
QY 142 GluGlyIleThrTyrArgGluTTPAlaProGlyAlaHisSerAlaAlaLeuValGlyAsp 161
Db 687 GAAGGTATCACTTACCGAATGGGCTCCTGAGCAGATTCGACGACATTAGTTGGCGAC 746
QY 162 PheAsnAsnTPAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTyrGlu 181
Db 747 TTCAACATTTGGATCCAAATGACAGACCATATAGCAAAATATGACTTGGTTGGAG 806
QY 182 IlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValLys 201
Db 807 ATTTTTCGCAACAAACATGAGATGTTGGCCACCAATTCCTCAGCGCTCAGCGGGAAG 866
QY 202 IleArgMetAspThrProSerGlyValLysAspSerIleSerAlaTTPIleLysPheSer 221
Db 867 GTGGAATGGATCTCCATCTCGGATTAAGATTCATATTCGCTTGATCAAGTCTCC 926
QY 222 ValGlnAlaProGlyGlnIleProPheAsnGlyIleTyrTyrAspProProGluGlnIle 241
Db 927 GTGACAGCTCCAGAGATATCCATATACATGGAATATATTAAGATCTCCAGAGAGAG 986
QY 242 LysTyrValPheGlnHisProGlnProLysArgProGluSerLeuArgGlyIleTyrGluSer 261
Db 987 AAGATATGATTCAGACATCCCTCAACCTTAAGCACAATATCTGGGATATATGAACA 1046
QY 262 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGlu 281
Db 1047 CATGTTGGCAAGATGAGCCGCAACCAAGATCAACATATGACAACTTCGGGGATGAG 1106
QY 282 ValLeuProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnIle 301
Db 1107 GTGCTTCCAAATATTAAGACTTGGATTCGATACAGTACAGTCCAAATATATGCAATCCAAG 1166
QY 302 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheIleProSerSerArg 321
Db 1167 CACTCATACATGGAAGCTTTGGGTACCATGTTACCAATTTCTTGGACCAAGTACCGG 1226
QY 322 PheGlyThrProGluAspLeuLysSerIleLeuPheArgAlaHisGluLeuGlyLeuLeu 341
Db 1227 TTTGGGTCGCCAGAGATTTTAAATCTTTGATTTGATTAAGCTCAGACAGCTTGGCTTGAT 1286
QY 342 ValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGly 361
Db 1287 GTCTCATGATGTGTTTTCACAGTCACCGCTCAATATATCTTGGACCGGTTGAATGGT 1346
QY 362 PheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisIleTTPMetTTP 381
Db 1347 TTTGATGCAAGATACATTAATCTTCATGCGGTTTCCATGCGGATCATCGAGATGG 1406
QY 382 AspSerArgLeuPheAsnTyrGlySerTTPGlyValIleLysArgPheLeuLeuSerAsnAla 401
Db 1407 GATTCGCCGTGTTTAACTATGAGGATTAAGAAAGTTAAGGTTCTACTTCCCAATGCA 1466
QY 402 ArgTTPThrLeuGluGlnTyrTyrLysPheAspGlyPheArgPheAspGlyValIleThrSerMet 421
Db 1467 AGATGTCGCTAGAGAGATATAGTTTATGCTTCCGATTCGATGCGCGACCTCATG 1526
QY 422 MetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyIleTyrPheGly 441
Db 1527 ATGTATACCATCATGAGTTTCAAGTACCTTACAGAGATACCATCAATATATTTTGGC 1586
QY 442 PheAlaThrAspValHisValValValTyrIleMetIleValIleAsnAsnIleIleHisGly 461

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Db      1587 TTTGCCCTGATGATGATGCGGCTGTTTACTTGATGCTGATGATGATCTAATTCATGCG 1646
QY      462 LeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIle 481
      1647 TTTTATCTCGTAGAGCGCTAATCATCGGTGAGATGTTAGTGAATGCCATCACTTTGCCCTT 1706
QY      482 ProValProAspGlyGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAspLys 501
      1707 CCGTGTAAAGTGGTGGGCTGGTTTGATGATGCTTACATATGAGCTGGTGGCCAGCA 1766
QY      502 TrpIleGluLeuLeuLysGlnSerAspGluSerTrpLysMetGlyAspIleValHisThr 521
      1767 TGGATTAACTCTCCAAAGAAAGATGAGTGAAGCTGGAGAGGGAATATGTCACACA 1826
QY      522 LeuThrAsnArgArgTrpLeuGluLysCysValThrTyrAlaGluSerHisAspAla 541
      1827 CTAAACAACAGAAAGTGGCTGAAAAGTGTACTTATGCTGAAGTCACGATCAGCA 1886
QY      542 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 561
      1887 CTGTGTGAGACAGACACTATTCATCTGTGATGACAAAGATATGATATTCATG 1946
QY      562 AlaLeuAspArgProSerThrProArgIleAspArgIleAlaLeuHisIleMetIle 581
      1947 GCGCTGAACGACCTTCGACCCCTAATTCATGATCGTGAATATGCACTGCATTAATGATT 2006
QY      582 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 601
      2007 AGACTTATCAACAAGGCTCTAGAGAGAGAGGCTTACTTACTTATGGAATAGATTTC 2066
QY      602 GlyHisProGluTrpIleAspPheProArgIleProGlnThrLeuProThrGlyLysVal 621
      2067 GGGCATCTCGATGATGATGACTTTCACAGAGCCCAAGATCACTTCACAGTGAAGTTTC 2126
QY      622 LeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgPheAspLeuGlyAspAla 641
      2127 ATCCCAAGAAACAAACAACAGTTTACACAAATCCCTCCAGATTTGACCTGGATATGCA 2186
QY      642 AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
      2187 GAATTTCTTAGCTATCATGTATGATGACAGATTTGATCAGGCAATGACAGATCTTGAGAA 2246
QY      662 LysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGlnGluAspLys 681
      2247 AAATATGTTTATGACATCAGACCAACAGTACGTATCTCGGAACATAGAGAAATAG 2306
QY      682 ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisIleTrpSerAsnSer 701
      2307 GTGATCGCTGTGAAAAGGGGACTTGATTTGTGTTCAATTCACACTGGAGTAGTAC 2366
QY      702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAspSer 721
      2367 TATTTGACTACCGGCTCGCTGTTTAAAGCTGGAGATACAGAGTGGTCTTAGACTCG 2426
QY      722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741
      2427 GACGCTGACCTTTGGTGGATTTGGTAGATCCATCACTGACAGACGACGCTCACTTCT 2486
QY      742 GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761
      2487 GACTGCCCAACATGACAACAGGCCCATTCATCTCAGTATCACTCTGACGAACCTGT 2546
QY      762 ValValTyrAla 765
      2547 GTTGCTATGCT 2558
Db

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RESULT 4
AAQ73750 standard: cDNA to mRNA; 2919 BP.
XX AAQ73750;
XX
XX

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DT      05-JUL-1995 (first entry)
DE      Rice starch branching enzyme.
XX      Starch branching enzyme; rice; starch content; ds.
XX      Oryza sativa.
XX      Key
FH      Location/Qualifiers
FT      5'UTR
FT      1..127
FT      /tag= a
FT      transic_peptide 128..322
FT      /tag= b
FT      mat_peptide 323..2606
FT      /tag= c
FT      /product= "branching_enzyme"
FT      3'UTR
FT      2603..2919
FT      /tag= d
PN      JP06261767-A.
XX      20-SEP-1994.
PD      22-OCT-1993; 93JP-00265171.
XX      29-OCT-1992; 92JP-00291719.
XX      (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
XX      MPI; 1994-337418/42.
XX      P-PSDB; AAR60811.
DR      New gene of branching enzyme of rice starch - useful for increasing
PT      starch yield of grain.
PS      Claim 1; Page 9-12; 13pp; Japanese.
XX      The rice starch branching enzyme is encoded by the cDNA sequence
XX      CC AAQ73750. The starch content of rice grains can be increased by
XX      CC increasing the expression of branching enzyme in rice plants
XX      SQ Sequence 2919 BP; 755 A; 590 C; 800 G; 774 T; 0 U; 0 Other;

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Alignment Scores:

Prod. No.:	Length:	Matches:	Score:
1.3e-308	2919	3362.00	602
Percent Similarity:	89.10%	Conservative:	68
Best Local Similarity:	80.05%	Mismatches:	72
Query Match:	80.64%	Indels:	10
DB:	2	Gaps:	2

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US-09-508-377-12 (1-768) x AAQ73750 (1-2919)
QY      17 ProAlaAlaIleGlnProGluGluLeuGlnIleProGluAspIleGluGlnThrAla 36
      377 CCGGTTTCAGACAGTTTCAGATCTGACAGTTCAGCTTATGATGAAATTAAGCAGC 436
QY      37 GluValAsnMetThrGlyGlyThrAlaGluLysLeuSerSerGluProThrGlnGly 56
      437 GAGGTT-----GAGCTGAAGTTGAGTTAGTATCTGGAGCAAGTAC--- 481
QY      57 IleValGluThrIleThrAspGlyValThrLysGlyValLysGluLeuValAlaGlyGlu 76
      482 -----GTTGAAGGCGTGAAGAGAGTGGTTGAAGATTGACTGCTGAGCAG 526
QY      77 LysProArgValAlaProLysProGlyAspGlyLysIleTyrGluIleAspProThr 96
      527 AAACCAAGAGTTGCTCCCAACAACAGAGATGGGCAAAAATATTCACAGATGACTCTATG 586
QY      97 LeuLysAspPheAspSerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAla 116
      587 CTTAATGCGTATATGATCATCTTGAATATGATATGATGATGATGATGATGATGATGATGAT 646

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Cy 117 AAlaIleAspGlnHisGluGlyGlyLeuGluAlaPheSerArgIleTyrGluLeuGly 136
 |||||:::|||||
 Db 647 GACATTTGATCAGATATGAGAGAGACGTGAAACATTTTCTCGCGGTATGAGAAATTGGA 706
 Cy 137 PheThrArgSerAlaGluGlyIleThrTyrArgGluThrAlaProGlyValHisSerAla 156
 |||||:::|||||
 Db 707 TTAAATCACAAGTGTCTAAGGTGTCACTTATCGAAGATGGCTCCCGGGGACATTTCTGCA 766
 Cy 157 AlaLeuValGlyAspPheAsnAsnThrPaspProAsnAlaAspThrMetThrArgAspAsp 176
 |||||:::|||||
 Db 767 GCATTAAGTAGGTGACCTTCAACAATTGGAAATCCAAATTCAGACCCGCAAGACAAATAAGAG 826
 Cy 177 TyrGlyValTyrGluIlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHis 196
 |||||:::|||||
 Db 827 TTGGGTGTTGGAGAGATTTTCTGCTTAACAATGCTGATGCTCATCTCTATTCCACAT 886
 Cy 197 GlySerArgValIleAlaArgMetAspThrProSerGlyValIleAspSerIleSerAla 216
 |||||:::|||||
 Db 887 GGCTACCGTGAAGAGGTGGAAATGGAATCCCATCTGGTAATAAGATTTATTTCTGCGC 946
 Cy 217 TPRIleLysPheSerValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAsp 236
 |||||:::|||||
 Db 947 TGGATCAAGTACTCTGTGCAAGCCGAGAGAAATCCCATACAAATGGAATATATTTATGAT 1006
 Cy 237 ProProGluGluGluIleTyrValPheGlnHisProGlnProLysArgProGluSerLeu 256
 |||||:::|||||
 Db 1007 CCTCTGGAAGAGAGATACATATTCAAGCATCTTCAACCTTAAGACCAAAAGTCATTTG 1066
 Cy 257 ArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrAla 276
 |||||:::|||||
 Db 1067 CGGAATATGGAATCATGTGTGGATAGATGACACCGAGCCAAAGATCAACAGTATGCA 1126
 Cy 277 AsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsnAlaValGlnIle 296
 |||||:::|||||
 Db 1127 AACTTTAGGGAAGAGGTCTTCCAGATCAAAAAGCTTGATGATCAATGCAGTGCATAA 1186
 Cy 297 MetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhe 316
 |||||:::|||||
 Db 1187 ATGGCAATTCAGAGCATCATATTATGGAAGCTTTGGTACCATGTCACCAATTTCTTT 1246
 Cy 317 AlaProSerSerArgPheGlyThrProGluAspLeuLysSerIleAspArgAlaHis 336
 |||||:::|||||
 Db 1247 GCACCAAGATGATCGTTCCGGAGCCCAAGATTTAAAGTCATTTGATGATTAAGATTCAT 1306
 Cy 337 GluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeu 356
 |||||:::|||||
 Db 1307 GAGCTTGGTTAGTTGTCTCATGATGTGTTTTCACAGCCATGCCGTCAATTAATACCTTA 1366
 Cy 357 AspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGly 376
 |||||:::|||||
 Db 1367 GATGGGTGGAACGGTTTATGGTACAGATACGCATTTACTTCAATGATGGTTCACGCGGC 1426
 Cy 377 HisHisTyrMetTyrAspSerArgLeuPheAsnTyrGlySerTyrGluValIleAsnArgPhe 396
 |||||:::|||||
 Db 1427 CATCATTTGATGGGATTTCTGCCCTTTTCAACTATAGGGAATGGGAAGTTCTAAGATTT 1486
 Cy 397 LeuLeuSerAsnAlaArgTyrTyrLeuGluGluTyrLysPheAspGlyPheArgPheAsp 416
 |||||:::|||||
 Db 1487 CTACTATCCAAAGCAAGATGGTGGCTCGAGAGATTAAGTTGATGGTTTCAAGATTTGAC 1546
 Cy 417 GlyValThrSerMetMetTyrThrHisGlyLeuGlnMetThrPheThrGlyAsnTyr 436
 |||||:::|||||
 Db 1547 GGTGTAACTCATGATGATCACTCATCATGATTCAGATTCAGATTAAGTAACTTAC 1606
 Cy 437 GlyGluTyrPheGlyPheAlaThrAspValAlaAspAlaValValTyrLeuMetLeuValAsn 456
 |||||:::|||||
 Db 1607 AGTGAATATCTTTGATTTGCCCATGATGCTGATGATGATGATTTACTTGAAGCTGGTAAAT 1666
 Cy 457 AspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGluAspValSerGlyMet 476
 |||||:::|||||
 Db 1667 GATTATATTCATGAGATTTATATCTGAGGCCATTAACCATCGTGAAGATGTCAAGTGAATG 1726
 Cy 477 ProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyrArgLeuHisMet 496

Db 1727 CCTACATTTGCCCTTCTCTTCACAGATGGTGGGAGTTGGTTTGGATATATGCGCTTCATATG 1786
 |||||:::|||||
 Cy 497 AlaValAlaAspIleTyrIleGluLeuLysGlnSerAspGluSerTyrPheMetGly 516
 |||||:::|||||
 Db 1787 GCTGTCTCTGACAAATGGATTTGATCTCTCAAGCAAAAGATGATGATCTTGGAAAGAGGT 1846
 Cy 517 AspIleValHisThrLeuThrAsnArgArgTyrPheGluLysCysValThrTyrAlaGlu 536
 |||||:::|||||
 Db 1847 GATATTTGACACACCTGACTACAGAAAGTGTGTAGAGAAAGTGTCTTATGCTTGAA 1906
 Cy 537 SerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheThrPheMetAspValAsp 556
 |||||:::|||||
 Db 1907 AGTCATGATCAAGCACTAGTGTGTACAAACTATGTGCTTCTGTTGATGGCAAGAT 1966
 Cy 557 MetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAla 576
 |||||:::|||||
 Db 1967 ATGTAATGATTTTATGCTCTTGACACAGCCGCAACCTTACATTTATCTGGAATAGCA 2026
 Cy 577 LeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPhe 596
 |||||:::|||||
 Db 2027 TTGCATAAATGATTAAGATTAATCAATGAGGCTTAGAGAGAGAAAGCTATCTTAATCTTT 2086
 Cy 597 MetGlyAsnGluPheGlyHisProGluTyrIleAspPheProArgGlyProGlnThrLeu 616
 |||||:::|||||
 Db 2087 ATGGAAATGAGTTCCGACATCTGAAATGATTTTCCAAAGACTCCACAAATGACTT 2146
 Cy 617 ProThrGlyLysValLeuProGlyLysAsnAsnSerTyrAspLysCysArgArgPhe 636
 |||||:::|||||
 Db 2147 CCAATGATTAATTCATCTCCAGGAAATACACAGTTATGATGAATGCGGTGCAAGATTT 2206
 Cy 637 AspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMet 656
 |||||:::|||||
 Db 2207 GACCTGGGTGATGGGACTATCTTATGATTCGTGATCGTGCATCTAGATTTGACCGCGGATG 2266
 Cy 657 GlnHisLeuGluGluIleTyrGlyPheMetThrSerGluHisGlnTyrValSerArgLys 676
 |||||:::|||||
 Db 2267 CAGCTCTCGAGGAAATATGGGTTTCATGATCAGACACACAGTATCTCGAAAG 2326
 Cy 677 HisGluGluAspLysValIleIlePheGluArgGlyAspLeuValPheValPheAsnPhe 696
 |||||:::|||||
 Db 2327 CATGAAGGATTAAGATATTAATTTTGAAGAGAGATCTGTATTTGTGTTCACTTC 2386
 Cy 697 HisTyrPheAsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLys 716
 |||||:::|||||
 Db 2387 CATGGAGTAAACAGCTATTTTGACTACACGCTGTGTTGTTTAAAGCAAGAAATATTAAG 2446
 Cy 717 ValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspVal 736
 |||||:::|||||
 Db 2447 GTGGCTTTGACTCAGAGCTGAGCTCTTGTGTGATTTGGCAGAGATCCATCACTGCA 2506
 Cy 737 AspTyrPheThrThrGlnHisProHisAspAsnArgProArgSerPheSerValTyrThr 756
 |||||:::|||||
 Db 2507 GAGCACTTCACTGCCGATTTGTTACATACACAGGCCCTACTCTGTTCAAGTTATTC 2566
 Cy 757 ProSerArgThrAlaValValTyrAlaLeuThrGlu 768
 |||||:::|||||
 Db 2567 CCTAGCAAGAACCTGGTGTCTATGCTCAAGGGAA 2602
 |||||:::|||||
 RESULT 5
 AAH78342
 ID AAH78342 standard; cDNA; 2968 BP.
 XX
 AC AAH78342;
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of wheat starch branching enzyme (BE1b).
 XX
 KW Wheat; starch branching enzyme; BE1b; SBE; transgenic plant;
 KM starch biosynthetic pathway; amylopectin; amylose; ss.
 XX
 OS Triticum sp.

XX WO200162934-A1.
 PN 30-AUG-2001.
 PD
 XX 21-FEB-2001; 2001WO-AU000175.
 PF 21-FEB-2000; 2000AU-00005742.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (GOOD-) GOODMAN FIELDER LTD.
 PA (LIMA-) GRP LIMABRAIN PACIFIC PTY LTD.
 XX
 PI Morell M, Rahman S;
 PI
 DR WPI; 2001-570635/64.
 XX
 PT Nucleic acids encoding wheat starch branching enzyme IIb, useful for
 PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
 PT and barley.
 PS
 PS Claim 6; Fig 9; 103pp; English.
 XX
 CC The present sequence encodes a wheat starch branching enzyme, designated
 CC BEIIB. BEIIB is a type II starch branching enzyme (SBE). The BEIIB
 CC nucleic acids may be used to genetically transform cereal plants such as
 CC wheat or barley and for altering their nutritional content by modulating
 CC the starch biosynthetic pathway to vary levels of amylopectin and/or
 CC amylose produced in the plant
 XX
 SQ Sequence 2968 BP; 784 A; 626 C; 796 G; 756 T; 0 U; 6 Other;
 SQ
 Alignment Scores:
 Pred. No.: 1.03e-307 Length: 2968
 Score: 3352.00 Matches: 606
 Percent Similarity: 89.01% Conservative: 74
 Best Local Similarity: 79.32% Mismatches: 70
 Query Match: 80.40% Indels: 14
 Gaps: 4
 US-09-508-377-12 (1-768) x AAH78342 (1-2968)
 QY 7 SerGlyAlaThrPheLeuGlyValAlaIArgProAlaAlaIaGlnPro----- 22
 DB 419 AGTGGCGGAAACA-----CCGCCCTTCATGACGGTCCCGTTCAGTTGAT 463
 QY 23 ---GluGluLeuGlnIleProGluAspIleGluGluGlnThrAlaGluValAsnMetThr 41
 DB 464 TCTGATGATCTGAAGTCCCA---TTCATTGATGATGAACA-----AGCCTACAG 511
 QY 42 GluGlyThrAlaGluLeuGluSerSerGluProThrGlnGlyIleValGluThrIle 61
 DB 512 GATGAGGTGAAGATGATTTGGCTTCAGAGACAAATCAGGTAGTGAAGAAATGAT 571
 QY 62 ThrAspGlyValThrIleGlyValIleGlyValIleValIleGlyIleProAspVal 81
 DB 572 GCTGAAGACACGACGATGACAAAGATCATCTACAGAGGAGAAATTACGCATTCTG 631
 QY 82 ProLysProGlyAspGlyGlnIleGlyIleGlyIleAspProThrLeuLysAspPheArg 101
 DB 632 CCACACCGGGAAATGACAGCAAAATATACGAGATTGACCAACGCTCCGACATTAAAG 691
 QY 102 SerHisLeuAspTyrArgTyrSerGlyTyrArgArgIleArgAlaIleAspGlnHis 121
 DB 692 TACCACTCTTGAGTATCGATATAGCTTATACAGGAGATAGCTTACAGCATGTAGAAC 751
 QY 122 GluGlyGlyLeuGluIlePheSerArgGlyTyrGlyLeuGlyPheThrArgSerAla 141
 DB 752 GAAGAGGAGATGATATTTTCCCGGCTTACGAAAGATTGGATTATGCCACAGGCT 811
 QY 142 GluGlyIleThrTyrArgGluTTPAlaProGlyAlaHisSerAlaIleValIleValAsp 161

QY 162 PheAsnAsnTTPAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTPGlu 181
 DB 872 TTCACAAATTGGATCCAAATGACACCATATGACAAATAATGACCTTGCTGGAG 931
 QY 182 IlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIys 201
 DB 932 ATTTTCTCGCAAAACATGACAGATGGTCCCAACCAATTCCTCCACGCGTCAAG 991
 QY 202 IleArgMetAspThrProSerGlyValIleAspSerIleSerAlaTPilePheSer 221
 DB 992 GTCCGATGGGTCTCCATCTGGGACCAAGATTAATCTCGTTGGATCAAGTACTCC 1051
 QY 222 ValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProGluGlu 241
 DB 1052 GTCCACACTCCAGAGATATACATACATGATATATATATATATATATATATATAT 1111
 QY 242 LysTyrValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrGluSer 261
 DB 1112 AAGTATGATTCACAGCATCCTCAACCTAAACGACCAAAATCATTCGATATAGAAC 1171
 QY 262 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGlu 281
 DB 1172 CAGTTGGCATGAGTAGCCCGGAACCAAGATCAACATATGCAACTTCAGGGATGAG 1231
 QY 282 ValLeuProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGlu 301
 DB 1232 GTCTTCCAAAGATTAAACATTTGATATATAGAGTCCACGAGCTCGCTTGCT 1291
 QY 302 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArg 321
 DB 1292 CACTCATCATATGAAAGCTTTGGGTACCATGTTCCAAATTTCTTGGCACCAAGTAGCCGT 1351
 QY 322 PheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeu 341
 DB 1352 TTGGGCTCCCAAGATTAAATCTTGATATATAGAGTCCACGAGCTCGCTTGCT 1411
 QY 342 ValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGly 361
 DB 1412 GTCTCATGATGATGTGTTCACAGTCACGCGCATATATACCTTGAGAGGGTTGATGCT 1471
 QY 362 PheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisHisTyrMetTrp 381
 DB 1472 TTGATGACGAGATACATACATTCCTCCATGCGCGTCCACGCGGCATCATGTGAG 1531
 QY 382 AspSerArgLeuPheAsnTyrGlySerTrpGluValLeuArgPheLeuLeuSerAsnAla 401
 DB 1532 GATTCCTCGTGTGTTAACTATGGAATAGGAAGTTATAGCTTCTCTTCCATGCA 1591
 QY 402 ArgTyrTrpLeuGluGluTyrLysPheAspGlyPheArgPheAspGlyValThrSerMet 421
 DB 1592 AGATGGGGCTAGAGCATTAATGATGATGTTCCGATTCGATGCGCGACCTCCATG 1651
 QY 422 MetTyrThrHisHisGlyLeuGluMetThrPheThrGlyAsnTyrGlyGluTyrPheGly 441
 DB 1652 ATGATATCCCATCATGATTAACAAGTAACTTTACAGAACTTACAGAACTTACATGATTTTGGC 1711
 QY 442 PheAlaThrAspValAlaAspAlaValTyrLeuMetLeuValAsnAspLeuIleHisGly 461
 DB 1712 TTGGCCCTAGTAGATAGCGGTGCTTACTTGAATGCTGATGATGATGATGATGATG 1771
 QY 462 LeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIle 481
 DB 1772 TTTTATCTGAAGCGTAACATCATGCGTAAGATGTAGTAAGATGCTTACATTCCTCCT 1831
 QY 482 ProValProAspGlyGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAspLys 501
 DB 1832 CCTGTTCAAGTTGGTGGGTTGTTTGAATATGCTTACATATGCGTGTGCGCGCAAA 1891
 QY 502 TrpIleGluLeuLeuLysGlnSerAspGluSerTrpLysMetGlyAspIleValHisThr 521
 DB 1892 TGGATTAACTTCCAAAGCAACGATGAGCTTGAGAGATGGGATATATTTGCAACA 1951

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QY 522 LeuThraenaArgTrpLeuGluYsCyValThrTyraGluSerHisAspGlnAla 541
Db 1952 CTAACAAACAGAGGTGGCTGGAAAAGTGTGTTACTTATGCGAAAGTCACGATCAAGCA 2011
QY 542 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysPheTyrAspPheMet 561
Db 2012 CTGTGTGAGACACAGACTATGTCATTCGTGTGATGAGACAGATATGATGATTCATG 2071
QY 562 AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisIleSerMetIle 581
Db 2072 GCGCTGAACGAGACCTTCGACCGCTATATGATTCGTGGAATGACATGCAATAAAAGATT 2131
QY 582 ArgLeuValIleMetGlyLeuGluGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 601
Db 2132 AGACTTATCACACATGGGTCTAGAGAGAGGGTATCTTAACCTTATGGGAAATGAGTTC 2191
QY 602 GlyHisProGluTrpIleAspPheProArgGlyProGlnIleLeuProThrGlyLysVal 621
Db 2192 GGGCATCCTGATGATGATGACTTCCAGAGGCCCAACAGTACTTCCAGGTGATAGTTC 2251
QY 622 LeuProGlyAsnAspAsnSerTyrAspLysCysArgArgPheAspLeuGlyAspAla 641
Db 2252 ATCCAGGAAACAAACACGTTACGACAAATGCCGTCGAGATTTCACCTGGGTGATGCA 2311
QY 642 AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
Db 2312 GAATTTCTTAGGATCATAGTATGACAGAGAGTTCATGATCAGCAATGACAGCATCTTGAGAA 2371
QY 662 LysTyrGlyPheMetThrSerGluHisGlnTyrValSerArgLysHisGluGluAspLys 681
Db 2372 AAATATGGTTTATGACATCAAGACCAACAGTACGTATCTCGGAAACATAGAGAAATAG 2431
QY 682 ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheIleTrpSerAsnSer 701
Db 2432 GTGATTCGTTTGAAGAAAGGAGCTTGATTTTGTTCACTTCACCTGGAGTAGTAGC 2491
QY 702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAspSer 721
Db 2492 TATTTCCGACTACCGGGCTGGCTGTTAAAGCCTGGGAATCAAGGTGCTTAGACTGC 2551
QY 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741
Db 2552 GACGCTGACCTCTTTGGTGGATTTGTAGGATCCATCACTGACAGAGCATTCACCTCT 2611
QY 742 GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761
Db 2612 GACTGCCAACATGACACAGGCCCATTTCTCTGATCTGATCACTCTAGACAGAACCTGT 2671
QY 762 ValValTyrAla 765
Db 2672 GTGTCTATGCT 2683

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RESULT 6
ID AAV70961 standard; DNA; 2640 BP.
XX
AC AAV70961;
XX
DT 23-AUG-1999 (first entry)
XX
DE DNA encoding maize branching enzyme II.
XX
KW Non-glycogen-like polysaccharide production; fermentation;
KW starch synthase enzyme; glycogen-synthesis enzyme; glycogen synthesis;
KW non-starch branching gene; amylopectin; amylose; plant-like starch;
KW maize branching enzyme II; ss.
XX
OS Zea mays.
XX
PN MO9844780-A1.
XX
PD 15-OCT-1998.
XX

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PF 03-APR-1998; 98WC-US006660.
XX
XX 04-APR-1997; 97US-0042939P.
XX
XX (EXSE-) EXSEED GENETICS LLC.
XX
PI Guan H, Keeling PJ,
XX
XX WPI: 1998-568285/48.
XX
DR P-PSDB; AAV70961.
XX
XX
PT Producing non-glycogen-like polysaccharides in bacteria, fungi or plants
PT - transformed with genes for enzymes involved in starch or glycogen
PT synthesis allows fermentative production of starches with engineered
PT properties.
XX
PS Disclosure; Fig 53; 150pp; English.
XX
XX The specification describes a method for the production of non-glycogen-
XX like polysaccharides in a host. The method comprises transforming a host,
XX suitable for fermentation, with genes encoding starch- or glycogen-
XX synthesis enzymes, and fermenting the transformants. The specification
XX also describes hosts transformed with a gene active in glycogen synthesis
XX and at least one non-starch branching gene, involved in production of
XX amylopectin or amylose in its original host. The method is used to
XX produce plant-like starches by fermentation and new starches in plants.
XX These starches are useful for all food and non-food applications of
XX starch. The present sequence is used in the course of the invention
XX
SQ Sequence 2640 BP; 715 A; 510 C; 686 G; 729 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,086-307 Length: 2640
Score: 3351.00 Matches: 609
Percent Similarity: 87.24% Conservative: 68
Best Local Similarity: 78.48% Mismatches: 77
Query Match: 80.38% Indels: 22
DB: Gaps: 4
US-09-508-377-12 (1-768) x AAV70961 (1-2640)
QY 4 PheAlaValSerGlyAlaThrLeuGlyVal-----AlaArgProProAla 18
Db 108 TTCTTAACCTCGGGGTGCTCGAGTGGATGTCGCGGACGACGCGCATGCGCGCGG 167
QY 19 AlaAlaGlnProGluGluLeuGlnIleProGluAspIleGluGluThrAlaGluVal 38
Db 168 GCCGGCCGACAGAAAGCGGTGATGATGTTCTGAGGCCGCAAAATGAT----- 212
QY 39 AsnMetThrGlyGlyThrAlaGluLysLeuGluSerSerGlu----- 52
Db 213 -----GGCTCGCATCAAGGGCTGACTCGCTCATTCAGTCGATGAGTACTG 260
QY 53 ProThrGlnGlyIleValGluThrIleThrAspGlyValIleLysGlyValLysGluLeu 72
Db 261 GAGGTACACAGACATTTCTGAAGAGACAAACGCGGTGCT-----GGTGTGCTATGCT 314
QY 73 ValValGlyGluLysProArgValValProLysProGlyAspGlyGlyLysIleTyrGlu 92
Db 315 CAAGCCTTGAACAGATTCGATGCTGCTCCCGCCACCAACGATGACAAAAATATTCGAG 374
QY 93 IleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGluTyrArg 112
Db 375 ATTAGACCCCATGTTGACAGGCTATTAAGACATCTTGATGCTAGCTAGCCTCATAGA 434
QY 113 ArgIleArgAlaAlaIleAspGlnHisGluGlyGlyLeuGluAlaPheSerArgGlyTyr 132
Db 435 AGAATCCGTTACAGCATGATGAGAACATGAGAGAGCTTGAGAACCTTCTCCGTGATAT 494
QY 133 GluLysLeuGlyPheThrArgSerArgGluGlyIleThrTyrArgGluTyrAlaProGly 152
Db 495 GAGAGTTTGGATTAAATCCGACCGCGGAGAGATACATATCGAAATGGCTCTCTGA 554

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QY	153	AlaHisSerAlaAlaLeuValGlyAspPheAsnMetTrpAsnProSerAlaAspThrMet	172
QY	154	AlaHisSerAlaAlaLeuValGlyAspPheAsnMetTrpAsnProSerAlaAspThrMet	173
Db	555	GCATTTTCGCAGCATGTGGGGTGACTTCACAACTGGGATCCAAATGCAGTTCGTATG	614
QY	173	ThrArgAspAspThrGlyValTrpGluIlePheLeuProAsnSerAlaAspGlySerPro	192
QY	174	ThrArgAspAspThrGlyValTrpGluIlePheLeuProAsnSerAlaAspGlySerPro	193
Db	615	ACGAAATAGAGTTGGGTGGGAAATTTTCTGCTCAACATGCAGATGGTATATCA	674
QY	193	AlaIleProHisGlySerArgValIysIleArgMetAspThrProSerGlyValIysAsp	212
QY	194	AlaIleProHisGlySerArgValIysIleArgMetAspThrProSerGlyValIysAsp	213
Db	675	CCATATTCCTCATGATCTCGTGTAAAGGTGAGATGATCTCCATCAGGGAGTAAAGAT	734
QY	213	SerIleSerAlaThrPheLeuPheSerValGlnAlaProGlyGluIleProPheAsnGly	232
QY	214	SerIleSerAlaThrPheLeuPheSerValGlnAlaProGlyGluIleProPheAsnGly	233
Db	735	TCATATTCACGCTGGATCCAAATGCTCACTGTCAGAGCCCCAGAGAAATACATATGATGG	794
QY	233	IleTyrTyrAspProGluGluGluIuLysTyrValPheGlnHisProGluProLysArg	252
QY	234	IleTyrTyrAspProGluGluGluIuLysTyrValPheGlnHisProGluProLysArg	253
Db	795	ATTATTAATGATCTCTCTGTAAGAGGTAAAGTATGTGTTTCAGCATGGCAACTTAAACGA	854
QY	253	ProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIle	272
QY	254	ProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIle	273
Db	855	CCAAATATCATTTGGGATATATGAAACAACAGTGGGATGATGAGCCGGAAACCGAATATA	914
QY	273	AsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsn	292
QY	274	AsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsn	293
Db	915	AACACCATATATACTTAAGGATGAGTCTCTCCAGAAATAAAAAATCTGGATACAT	974
QY	293	AlaValGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisVal	312
QY	294	AlaValGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisVal	313
Db	975	GCAGTGCAAATTAATGGCAATCCAAAGACATCATATTATGGAAGCTTGGATATCCATGTA	1034
QY	313	ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIle	332
QY	314	ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIle	333
Db	1035	ACPAATTTTTTTTGGCCAAAGTAGTGTTTTGGTATCCCAAGAAAGATTAAGATCTTTGATT	1094
QY	333	AspArgAlaHisGlyLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer	352
QY	334	AspArgAlaHisGlyLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer	353
Db	1095	GATAGACACATAGTGGCTTGTTGCTGATGTTCTCATGATGATGGTTCATATGATCAGCGCA	1154
QY	353	AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly	372
QY	354	AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly	373
Db	1155	AGTAATATCTCGTAGTGATGAAAGGTTTGATGTACAGATACATTAATCTTCAACAGT	1214
QY	373	GlyProArgGlyHisHisIleTrpMetTrpAspSerArgLeuPheAsnTyrGlySerTrpGlu	392
QY	374	GlyProArgGlyHisHisIleTrpMetTrpAspSerArgLeuPheAsnTyrGlySerTrpGlu	393
Db	1215	GGTCCAGGTGGCCATCAGTGGATGGGATTTCTGGCTATTAACTATGGGAATCGGGA	1274
QY	393	ValLeuArgPheLeuLeuSerAsnAlaArgTrpTrpLeuGluGluTyrLysPheAspGly	412
QY	394	ValLeuArgPheLeuLeuSerAsnAlaArgTrpTrpLeuGluGluTyrLysPheAspGly	413
Db	1275	GTTTTTAAGATTCTCTCTCTCCAAAGCTATGATGGTGGCTCGAGGAATATAAGTTGATGGT	1334
QY	413	PheArgPheAspGlyValIleThrSerMetMetTyrThrHisGlyLeuGlnMetThrPhe	432
QY	414	PheArgPheAspGlyValIleThrSerMetMetTyrThrHisGlyLeuGlnMetThrPhe	433
Db	1335	TTTCGGTTTGAATGGTGAACCTCCATGATGATACATCTACCGGATTTCAAGTAAACATTT	1394
QY	433	ThrGlyAsnTyrGlyGluTyrPheGlyPheAlaThrAspValAspAlaValIleTyrLeu	452
QY	434	ThrGlyAsnTyrGlyGluTyrPheGlyPheAlaThrAspValAspAlaValIleTyrLeu	453
Db	1395	ACGGGGAACTCATGATATTTTGGCTTTGGCACCATGATAGATGAGTGGTTACTTGG	1454
QY	453	MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGlnAsp	472
QY	454	MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGlnAsp	473
Db	1455	ATGCGGTAAATGATCTAATCATGATGATTTATCTGAGGCGTGAACATGGTGAAGAT	1514
QY	473	ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr	492
QY	474	ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr	493
Db	1515	GTTATGTGAATGCCATACATTTGCCCTCTCTGTTCACAGATGGTGGGATGTTTACATAT	1574
QY	493	ArgLeuHisMetAlaValAlaAspLysTrpIleGluLeuLeuLysGlnSerAspGlnSer	512
QY	494	ArgLeuHisMetAlaValAlaAspLysTrpIleGluLeuLeuLysGlnSerAspGlnSer	513
Db	1575	CGGATGCATATGAGCTGTGGCTGACAAATAGATTGATCTTCAAGCAAGATGATAAACT	1634

Db	1635	TGGAAAGATGGGTATATTGTGCACACACTGCAAAATAGAGGTGGTTAGAGAGTGTGTA	1694
QY	533	ThrTyrAlaGluSerHisAspGlnAlaLeuValGlyAspIysThrIleAlaPheTrpLeu	552
Db	1695	ACTATCTCTAAAGTCATGATGATCAAGCACTTGTGGCCACAGACATATGTGGTTGGTTG	1754
QY	553	MetAspIysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp	572
Db	1755	ATGGCAAGAGGTATGATGATTTTCATGTCGCTCGATAGACCTTCAGCTCCACGATTCAT	1814
QY	573	ArgGlyIleAlaLeuHisIleYsMetIleArgLeuValThrMetGlyLeuGlyGlyGly	592
Db	1815	CGTGGATAGCATTAACATTAAGATGATTAGACTTTCACAAATGGGTTTAGAGGAGAGAGGC	1874
QY	593	TyrIleuAsnPheMetGlyAsnGlnPheGlyHisProGluTrpIleAspPheProArgGly	612
Db	1875	TATGTTATTTTCATGGGAATAGATGTTTGGACATCTTGATGATGATGATTTCCAAAGGT	1933
QY	613	ProGlnThrIleuProThrGlyIysValIleuProGlyAsnAsnAsnSerTyrAspIysCys	632
Db	1935	CCGGAAGACTTCCAGAGGTGATTTATTCACAGGATATACACAGATTAGACAAAGTGT	1994
QY	633	ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnIlePhe	652
Db	1995	CGTCGAAGATTGTGACCTGGGTGATGACAGACATATCTTAGATTCATGGTATCCAAAGTTT	2055
QY	653	AspGlnAlaMetGlnHisLeuGlnGlyIleTyrGlyPheMetThrSerGlnHisGlnTyr	672
Db	2055	GATCAGGCAATGCCAATCATCTTGAGCAAAATATGATTCATGACATCGATCGATCCAGAT	2111
QY	673	ValSerArgIysHisGlyGlnAspIysValIleIlePheGluArgGlyAspLeuValPhe	692
Db	2115	ATTTCGCCGAAGCATGAGAGGATTAAGGTGATTGGTTCGAAAAGGAGATTGGTATTT	2174
QY	693	ValPheAsnPheHisTrpSerAsnSerPhePheAspTyrArgValGlyCysSerArgPro	712
Db	2175	GTGTTCAACTTCCACTGCACAAACAGCTATTTGACTACCGTATTTGGTTGCGAAAGCT	2233
QY	713	GlyIysTyrIysValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeu	732
Db	2235	GGGCGTATTAAAGTGTGCTTGGAATCCGACCGGTGATATTGGGATTTAGCAGGATTC	2294
QY	733	AspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgProArgSerPhe	752
Db	2295	CATCAGCGACGCGACGACCTTCCCGCGACACTGTTGTCATGATAAATGAGCCATATTC	2355
QY	753	SerValTyrThrProSerArgThrAlaValValTyrAlaLeuThrGlu	768
Db	2355	TGGATTATTACCAACAGCAAGAACATGTGTGCTATGCTCCAGCTGGAG	2402
RESULT 7			
AAV29757			
ID	AAV29757	standard; DNA; 2725 BP.	
AC	AAV29757;		
XX			
XX			
DT	11-SEP-1998	(first entry)	
XX			
DE	Zea mays	starch branching enzyme II gene.	
XX			
KW	SER; starch-encapsulating region; fusion vector;		
XX	starch branching enzyme II; ss.		
OS	Zea mays.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	91..2490	
FT		/tag= a	
FT	sig_peptide	/product= "starch branching enzyme II"	
FT		91..264	
FT		/tag= b	
FT	mat_peptide	265..2487	

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FT      /+tag= c
XX      WO9814601-A1.
XX
XX      09-APR-1998.
PD
XX      30-SEP-1997; 97WO-US017555.
XX      PF
XX      30-SEP-1996; 96US-0026855P.
XX      PR
XX      (EXSE-) EXSEED GENETICS LLC.
XX      PA
XX      Keeling P, Guan H;
XX      WPI, 1998-240100/21.
DR      P-PSDB; AAMS6489.
XX
XX      Hybrid polypeptide comprising starch-encapsulating region and protein -
PT      useful for, e.g. producing protein(s) resistant to degradation by stomach
PT      acids.
XX
XX      Example 2; Page 44; 156pp; English.
XX
XX      The sequence is that of the starch branching enzyme II gene. It can be
CC      used in the production of a hybrid polypeptide comprising a starch-
CC      encapsulating region (SER) fused to a payload protein. The hybrid
CC      polypeptide can be used to make modified starches comprising the payload
CC      protein, selected from, e.g. hormones, growth factors, antibodies,
CC      enzymes, dyes, immunoglobulins, etc. The modified starch can also be used
CC      to provide grain feeds enriched in amino acids. By encapsulating the
CC      payload protein in starch, it is more resistant to degradation by stomach
CC      acids.
XX
XX      Sequence 2725 BP; 727 A; 534 C; 715 G; 749 T; 0 U; 0 Other;
SQ

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Alignment Scores:
Pred. No.:      8.09e-307      Length:      2725
Score:          3342.00      Matches:      608
Percent Similarity: 86.98%      Conservative: 67
Best Local Similarity: 78.35%      Mismatches: 79
Query Match:      80.16%      Indels:      22
DB:              2          Gaps:      4

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US-09-508-377-12 (1-768) x AAV29757 (1-2725)

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QY      4 PheAlaValSerGlyValAlaThrLeuGlyVal-----AlaArgProProAla 18
DB      193 TTCTTAACCTCGGAGTCTCGAGTGGATGTTCCGGGAGCAGCAGGGGCCATGCGCGGCG 252
QY      19 AlaAlaGlnProGluGluLeuGlnIleProGluAspIleGluGluGlnThrAlaGluVal 38
DB      253 GCGCGGGCCAGAGAGGCGGTGATCGTTCCTGAGGGGAGAAATAT----- 297
QY      39 AsnMetThrGlyGlyThrAlaGluLysLeuGlnSerSerGlu----- 52
DB      298 -----GGCCTCCGATCAAGAGGCTGACTCGGCTCAATTCAGTCGATGAATG 345
QY      53 ProThrGlnGlyIleValGlnThrIleThrAspGlyValIleLysGlyValLysGluLeu 72
DB      346 GAGGTACCAAGACATTTCTGAAGAGACACCTGCGGCT-----GATGCGCTGATGCT 399
QY      73 ValValGlyGluLysProArgValValProLysProGlyAspGlyGlnLysIleTyrGlu 92
DB      400 CAAGCCTTAACAGAGATTCGAGTGGTCCCGCCCAACAAGCATGGAACAAAAATATTCAG 459
QY      93 IleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGluTyrArg 112
DB      460 ATTGACCCCATGTTGCAAGGCTTAAGTACCATCTTGAGTACGTTACAGCTCTTATAGA 519
QY      113 ArgTleArgAlaAlaIleAspGlnHisGluGlyGlyLeuGlnAlaPheSerArgGlyTyr 132
DB      520 AAGATTCGTTCAACATCTGATGAACATGAAGAGGCTTGAAGGCTTCTCCCGTATAT 579

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QY      113 GluLysLeuGlyPheThrArgSerAlaGluGlyIleThrTyrArgGluTyrAlaProGly 152
DB      580 GAGAGATTGGATTAAATGACCAGCGCGGAAGGATACATATGAGAAATGGCTCCGGA 639
QY      153 AlaHisSerAlaAlaLeuValGlyAspPheAsnMetTyrAspProMetAlaAspThrMet 172
DB      640 GCATTTTCGACGCAATGGTGGGTACCTCAACAATGGAGATCCAAATGCAATGCTATG 699
QY      173 ThrArgAspAspTyrGlyValTyrGluIlePheLeuProAsnAsnAlaAspGlySerPro 192
DB      700 AGCAAAATGAGCTTGGTGGTATTTTCTCCCTAACATGCAATGCGATGCTACATCA 759
QY      193 AlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAsp 212
DB      760 CCTATTCCTCATGATCTCGTGTAAAGTGAGAAATGATATCTCATCAGGAGTAAAGAT 819
QY      213 SerIleSerAlaTyrIleLysPheSerValGlnAlaProGlyGluIleProPheAsnGly 232
DB      820 TCAATTCAGCCTGGATCAAGTACTCAAGTCAAGGCCCCGAGGAAATACCATATGATGG 879
QY      233 IleTyrTyrAspProProGluGluGluLysTyrValPheGlnHisProGlnProLysArg 252
DB      880 ATTATTATGATCCCTCCGAGAGAGTAAAGTATGTGTTCAAGCATCCGCACTTAAACGA 939
QY      253 ProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIle 272
DB      940 CCAAAATCATTTGCGGATATATGAACAACATGCGGATAGTACCCCGGAACCGAAGATA 999
QY      273 AsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsn 292
DB      1000 AACCATATGTAAACTTTAAGGATGAAGTCCCTCCCAAGATTAATAAACTGGATCAAT 1059
QY      293 AlaValGlnIleMetAlaIleGlnGlnHisSerTyrTyrAlaSerPheGlyTyrHisVal 312
DB      1060 GCAGTGCAATATATAGCAATTCACAGACATCATATTATGAAAGCTTTGGATCCCATGTA 1119
QY      313 ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIle 332
DB      1120 ACTAATTTTGTTCGCGCAAGTATGCTGTTTGCTACCCCGAAGATTTGAAGTCTTGATT 1179
QY      333 AspArgAlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer 352
DB      1180 GATAGAGCAGATGAGCTTGTTGCTAGTCTCAAGATGTGATCATAGTCATAGTCAGGCTCA 1239
QY      353 AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly 372
DB      1240 AGTAATATCTCGATGGGTGATGATGTTTGAATGATACAGATACACATTAATCTTCACAT 1299
QY      373 GlyProArgGlyHisHisTyrMetTyrAspSerArgLeuPheAsnTyrGlySerTyrGlu 392
DB      1300 GGTCCAGCGGACCATCACTGATGATGGGATGTCCTCCCTATTAACTATGGGAACCTGGGA 1359
QY      393 ValLeuArgPheLeuLeuSerAsnAlaArgTyrTyrPheGluGlnGluTyrTyrPheAspGly 412
DB      1360 GTTTAAAGATTTCTTCTCCATGCTAGATGATGATGCTCGAGAGAAATTAAGTGTGATGAT 1419
QY      413 PheArgPheAspGlyValThrSerMetTyrThrHisHisGlyLeuGlnMetThrPhe 432
DB      1420 TTCCGTTTGAATGGGTGATACCTCCATGATGATACACTACACAGAGANTTACAGTAACATT 1479
QY      433 ThrGlyAsnTyrGlyGluTyrPheGlyPheAlaThrAspValAspAlaValLysTyrLeu 452
DB      1480 ACGGGGAATTCATGAGATATTTTGGCTTGGCACCGAAGTGAAGACATGGTTACTTG 1539
QY      453 MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyLysAsp 472
DB      1540 ATGCTGGTAATGATCTATATCATGATGATTTATCTCCAGAGCTGTAACTTGGTGAAGAT 1599
QY      473 ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr 492
DB      1600 GTTAGTGAATGCCATCAATTTGGCTTCTGTTACAGATGATGGGTAGTGTGATCTAT 1659

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Db 1660 CGGATGCATATGGCTGCTGACAAATGGATTGACCTTCTCAAGCAAGTATGAACT 1719
Qy 513 TTDlysmetGlyAspIleValHisThrLeuThrAspArgTrpLeuGluysCysVal 532
Db 1720 TGGAGAGTGGGTGATGATGTCACACTGACAAATAGAGGTGTGTAGAGAGTGTGA 1779
Qy 533 ThrTyralaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaThrPheLeu 552
Db 1780 ACTTATGCTGAAGACATGATCAACCATTTAGTCGGCGCAACAAACATTTGCGTTGGTGG 1839
Qy 553 MetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
Db 1840 ATGGCAAGAGATATGATGATTTGATGGCCCTCGATGACCTTCAACTCCATTCATTTGAT 1899
Qy 573 ArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGly 592
Db 1900 CGTGGGATAGCATTCATTAAGATGATTTGACTTATCAATGCGTTTACAGAGAGGCGC 1959
Qy 593 TyrLeuAspPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGly 612
Db 1960 TATCTTATTTTCATGGAAATGATGATTTGACATCTCGAATGATGATTTTCCAAAGAGT 2019
Qy 613 ProGlnThrLeuProThrGlyLysValLeuProGlyAsnAspAsnSerTyrAspLysCys 632
Db 2020 CCGCAAGACTTCCAAAGTGGTATTTATTCAGGGAATTAACAACAGTTATGCAATGT 2079
Qy 633 ArgArgAspPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnGluPhe 652
Db 2080 CGTGAAGATTTGACTGGGTGATGACATCTTATGATCATGCTTATTCAGAGGCTTT 2139
Qy 653 AspGlnAlaMetGlnHisLeuGluGluLysTyrGlyPheMetThrSerGlnHisGlnTyr 672
Db 2140 GATCAGGCAATGCAACATCTTGAGCAAAATATGATTCATGACATCTGATCCAGATAT 2199
Qy 673 ValSerArgLysHisGluGluAspLysValIleIlePheGluArgGlyAspLeuValPhe 692
Db 2200 ATTTCCCGGAACATGAGAGGATTAAGATTTGTTGGAAGAGGAGATTTGGATTT 2259
Qy 693 ValPheAspPheHisThrSerAsnSerPheAspTyrArgValGlyCysSerArgPro 712
Db 2260 GTGTTCAACTTCCACTGCACAAACAGCTATTTTGAATTCACGATTTGTTGCAAAAGCT 2319
Qy 713 GlyLysTyrLysValAlaLeuAspSerAspAlaLeuPheGlyGlyPheSerArgLeu 732
Db 2320 GGGGTGTAAAGTGATGCTTGGACTCCGACGCTGACATTTGGTGGAATTTACAGAGATC 2379
Qy 733 AspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgProAspSerPhe 752
Db 2380 CATCAGCAGACCGACACTTCCCGCGACTGTTCCAGATGATTAATGGCCATATTCATT 2439
Qy 753 SerValTyrThrProSerArgThrAlaValValTyrAlaLeuThrGlu 768
Db 2440 TCGGTTTATACCAAGACGAACATGTGTCTATGCTCCAGTGGAG 2487

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RESULT 8
AAT69729
ID AAT69729 standard; DNA; 2665 BP.
XX
AC AAT69729;
XX
DT 10-SEP-1997 (first entry)
XX
DE Plasmid pBE240 insert encoding corn starch branching enzyme IIb.
XX
KM Starch branching enzyme IIb, SBEIIb; corn, maize; antisense; amylopectin;
transgenic plant; pBE240; ss.
XX
OS Zea mays.
XX
Key Location/Qualifiers
FH 79..2478
FT CDS /*tag= a

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XX
PN MO9722703-A2.
XX
PD 26-JUN-1997.
XX
PF 12-DEC-1996; 96MO-US019678.
XX
PR 20-DEC-1995; 95US-0009113P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
XX
PI Hubbard NL, Klein TM, Broglie KE;
XX
DR WPI; 1997-341694/31.
XX
DR P-PSDB; AAW19212.
XX
PT Transgenic corn in which grain derived starch fine structure is
PT controlled - specifically branch chain distribution of amylopectin,
PT useful in preparation of chickened feedstuff.
XX
PS Example 1; Page 50-53; 92pp; English.
XX
CC A cDNA insert (AAT69729) in plasmid clone pBE240 comprises a 2.7 kb EcoRI
CC -XhoI fragment isolated from a corn cDNA library. It includes an open
CC reading frame encoding starch branching enzyme IIb (SBEIIb) (AAW19212).
CC The insert was used as a starting point in the assembly of DNA constructs
CC (see also AAT69730, AAT69736-37) designed to achieve suppression of
CC SBEIIb expression in transgenic corn plants, and thereby to produce novel
CC starches that have properties beneficial in food and industrial
CC applications
XX
SQ Sequence 2665 BP; 700 A; 525 C; 705 G; 735 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 9,766-307 Length: 2665
Score: 3341.00 Matches: 608
Percent Similarity: 86.98% Conservative: 67
Best Local Similarity: 78.35% Mismatches: 79
Query Match: 80.14% Indels: 22
DB: Gaps: 4
US-09-508-377-12 (1-768) x AAT69729 (1-2665)
Qy 4 PheAlaValSerGlyAlaThrLeuGlyVal-----AlaArgProProAla 18
Db 181 TTCTTAACCTCGGGGTGCTCGAGTGGATGTTCCGGGAGCAGCGGGCCATGCGCGGGG 240
Qy 19 AlaAlaGlnProGluGluLeuGlnIleProGluAspIleGluGluGlnThrAlaGluVal 38
Db 241 GCGCGCGCCAGGAAGCGGCTATGCTTCTCAAGGCGCAAGATGAT----- 285
Qy 39 AsnMetThrGlyGlyThrAlaGluLysLeuGluSerGlu----- 52
Db 286 -----GGCTCGGATCAAGGCGCTACCTCGCTCAATTCAGTCCGATGAACCTG 333
Qy 53 ProThrGlnGlyIleValGluThrIleThrAspGlyValThrLysGlyValLysGluLeu 72
Db 334 GAGGTACCAAGCAATTTCTGAAGAGCAACGTCGCTGCT-----GGTGTGCTGATGCT 387
Qy 73 ValValGlyGluLysProArgValValProLysProGlyAspGlyGlyLysIleTyrGlu 92
Db 388 CAAGCTTTGAACAGAGTTCCAGTGTCTCCCGCCACCAACGATGACCAAAATATTCGCG 447
Qy 93 IleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGluTyrArg 112
Db 448 ATTGACCCCATGTTGCAAGGCTATTAAGTACATCTTGGTATCGGTACAGCTCTATAGA 507
Qy 113 ArgIleArgAlaAlaIleAspGlnHisGluGluGlyLeuGluAlaPheSerArgGlyTyr 132
Db 508 AGAATCGGTTCAGCATGTGATGAACATGAAGAGGCTTGAAGCTTCCCGTGGTATAT 567
Qy 133 GluLysLeuGlyPheThrArgSerAlaGluGlyIleThrTyrArgGluTyrAlaProGly 152

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Db 568 GAGAAAGTTGATTTAAATGCCAGCCGGAGGATATCATATGCAATATGGGCTCCCTGGA 627
 Qy 153 AAlHISerAlaAlaLeuValGlyAspPheAsnAsnTyrAsnProAsnAlaAspThrMet 172
 Db 628 GCATTTTCGCGAGCATTTGGTGGTGACTTCAACATCGGGATCCAAATGACAGATCGATG 687
 Qy 173 ThrArgAspAspTyrGlyValTyrGluTyrPheLeuProAsnAlaAspGlySerPro 192
 Db 688 AGCAAAATAGAGTTGGTGTGGGAAATTTTCTGCTTAACATGACAGATGGATGCA 747
 Qy 193 AlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAsp 212
 Db 748 CCTATTCCTCCAGGATCTGCTGTAAAGGTGAGATGATCTCCATCAGGAGATTAAGAT 807
 Qy 213 SerIleSerAlaTyrIleLysPheSerValGlnAlaProGlyGluIleProPheAsnGly 232
 Db 808 TCAATTCAGCCTGGATCAAGTACTCAGTGCAGGCCCCAGAGAAATACCATATGATGGG 867
 Qy 233 IleTyrTyrAspProProGluGluGlyLysTyrValPheGlnHisProGluInProLysArg 252
 Db 868 ATTATATATGATCCCTCGTAAGAGGTAAAGTATGTGTTCAAGCATGCGCAACCTAAACGA 927
 Qy 253 ProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIle 272
 Db 928 CCAAAATCATTCGGGATATATGAACACATGTCGAATGAGTAGCCCGGAAACGAAAGTA 987
 Qy 273 AsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsn 292
 Db 988 AACACATATGTAACCTTTAGGATGGAAGTCTCCCAAGATTAATAAACTTGATACAT 1047
 Qy 293 AlaValGlnIleLeuValIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisVal 312
 Db 1048 GCAGTCAAAATATAGCAATCCAAAGACACTCATATATGAAAGCTTGATACCATGTA 1107
 Qy 313 ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLysSerLeuIle 332
 Db 1108 ACTAAATTTTTTGGCCCAATAGTCGTTTGGTACCCCAAGAAATTTGAACTTTGATT 1167
 Qy 333 AspArgAlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer 352
 Db 1168 GATAGAGCATATAGCTGGTTTGTCTAGTCTCATGATGTGCTCATAGCAGCCGCA 1227
 Qy 353 AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly 372
 Db 1228 AGAATATATCTGATGGTGTGAATGTTTGTGATGTGTACAGATACATTAATCTTACACGT 1287
 Qy 373 GlyProArgGlyHisHisTyrMetTyrAspSerArgLeuPheAsnTyrGlySerTyrGlu 392
 Db 1288 GGTCCACGGCCCATCTCGATGTGGATTCGCTGCTATTAACATAGGGAATCGGGA 1347
 Qy 393 ValLeuArgPheLeuLeuSerAsnAlaArgTyrTyrLeuGluGlyPheAspGly 412
 Db 1348 GTTTTAAGATTTCTCTCTCCATGCTAGATGGTGGCTCGAGGAATATAAGTTTATGCT 1407
 Qy 413 PheArgPheAspGlyValThrSerMetMetTyrThrHisGlyLeuGlnMetThrPhe 432
 Db 1408 TTCCTGTTTGTAGTGTGACCTCCATGATGTACATCCACCGGATTTCAAGTAACTTT 1467
 Qy 433 ThrGlyAsnTyrGlyLysTyrPheGlyPheAlaThrAspValAspAlaValValTyrLeu 452
 Db 1468 ACCGGGAACCTCAATGAGTATTTTGGCTTGGCACCGAATGATGAGTCACTGTTTACTTG 1527
 Qy 453 MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGluAsp 472
 Db 1528 ATGCTGTGAATATGATCTAATTCATGAGACTTAACTCTGAGGCTGATACCATTTGTAAGAT 1587
 Qy 473 ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr 492
 Db 1588 GTTAGTGAATGAGCTACATTTGGCTTCTGCTTCAAGATGTGGGTAGGTTTGTGCTAT 1647
 Qy 493 ArgLeuHisMetAlaValAlaAspLysTyrIleGlyLeuLeuLysGlnSerAspGluSer 512
 Db 1648 CGATGATATATGCTGTGGCTGACAAATGATTAACCTTTCTCAAGCAAAAGTATGAACCT 1707

Qy 513 TrrPlyMetGlyAspIleValHisThrLeuThrAsnArgArgTyrPheGluTyrCysVal 532
 Db 1708 TGGAAAGATGGGTGATATTTGTGCACACTGACCAATATAGAGGTGTTTAAAGAAATGTGTA 1767
 Qy 533 ThrTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTyrLeu 552
 Db 1768 ACTTATGCTGAAGTCAATGATCAAGCATTAATGTCGCGACAAAGACATATATGCGTTTGGTTG 1827
 Qy 553 MetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
 Db 1828 ATGCAAAAGATATGATATGATTTCAATGACCCCTCGATAGCCTTCAACTCCATGATGAT 1887
 Qy 573 ArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGly 592
 Db 1888 CGTGGGATAGCATTAATAGATGATTAATTAACCTTATCAATAGGTTTAAAGAGAGGCG 1947
 Qy 593 TyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTyrIleAspPheProArgGly 612
 Db 1948 TATCTTAATTTCAATGGGAATATGAGTTTGGACATCCTGAATGATATGATTTCCAAAGAGT 2007
 Qy 613 ProGluThrLeuProThrGlyLysValLeuProGlyAsnAsnAsnSerTyrAspLysCys 632
 Db 2008 CCGCAAGACTTCCAAAGTGTAAATTTATCCAGGGAATTAACAACGTTATATGACAAATGT 2067
 Qy 633 ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnGluPhe 652
 Db 2068 CGTGGAAATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATGTATGATGCAAGACTTT 2127
 Qy 653 AspGlnAlaMetGlnHisLeuGluGluLysValIleIlePheGlnArgGlyAspLeuValPhe 672
 Db 2128 GATCAGGAAATGCAACATCTTGAAGCAAAATATGATTCATGACATGATCAACAGATAT 2187
 Qy 673 ValSerArgLysHisGluGluLysValIleIlePheGlnArgGlyAspLeuValPhe 692
 Db 2188 ATTTCCCGGAAACATGAGAGAGATTAAGTATGTTGTCGAAAGGAGATTTGGTATTT 2247
 Qy 693 ValPheAsnPheHisTyrPheSerAsnSerPhePheAspTyrArgValGlyCysSerArgPro 712
 Db 2248 GTGTTCACCTTCCACTGCAACACAGCTAATTTGACTACCGATATGTTGTTTCCAAAGCTT 2307
 Qy 713 GlyLysTyrLysValAlaLeuAspSerAspAlaLeuPheGlyGlyPheSerArgLeu 732
 Db 2308 GGGGTGTATAGGTGCTTGTGACTCCGACGCTGACATTTTGGTATTTAGACAGATC 2367
 Qy 733 AspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgProArgSerPhe 752
 Db 2368 CATCAACGACCGAGACATTCACCGCCGACTGTCGATGATATAGGCCATATATTCATCC 2427
 Qy 753 SerValTyrThrProSerArgThrAlaValValTyrAlaLeuThrGlu 768
 Db 2428 TCGGTTTATACACCAAGCAACATGTGTGCTATATGCTCAAGTGA 2475

RESULT 9
 ADA71289
 ID ADA71289 standard, DNA; 2655 BP.
 AC ADA71289;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX
 XX Rice gene, SEQ ID 4612.
 DE
 XX
 XX Plant; bacterial infection; fungal infection; viral infection; rice;
 XX gene; de.
 XX
 OS Oryza sativa.
 XX
 XX WO2003000898-A1.
 FN
 XX 03-JAN-2003.
 PD
 XX 22-JUN-2001; 2001WO-18001.05.
 PF


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XX 22-JUN-2001, 2001WO-IB001105.
PR
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Kataagiri F, Quan S, Tao Y, Whitcham S, Xie Z, Zhu T, Zou G;
XX
XX WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
XX Claim 6; SEQ ID NO 4612; 899bp; English.
XX
XX The present invention relates to a method (M1) for identifying genes
XX involved in plant resistance or response to pathogenic infection. M1
XX comprises identifying a gene whose expression is significantly altered in
XX the incompatible interaction of plant gene expression relative to
XX expression of the gene in an uninfected plant, in a mutant plant that
XX does not express a gene associated with response to pathogenic infection,
XX or in a corresponding incompatible or compatible interaction. (M1) is
XX useful for conferring resistance to resistance or tolerance to a plant to
XX bacterial, fungal or viral infection. The present sequence was used to
XX illustrate the invention.
XX
SQ Sequence 2655 BP; 714 A; 529 C; 680 G; 732 T; 0 U; 0 Other;

Alignment Scores:
Pred. NO.: 2,096-306 Length: 2655
Score: 3337.50 Matches: 646
Percent Similarity: 77.09% Conservative: 44
Best Local Similarity: 72.18% Mismatches: 68
Query Match: 80.06% Indels: 139
DB: Gaps: 8

US-09-508-377-12 (1-768) x ADA71289 (1-2655)
QY 1 MetalathrPheAlaValSerGlyAlaThrLeuGlyValAlaArgPro----- 16
Db 1 ATGGCGTCGTTGCGCGGTCCGGCGGAGGCTCGGGGTGCGGGGGGGGGCGGCGG 60
QY 17 -----ProAlaAla----- 19
Db 61 GGCGGCGGCGGCGGGGTGGCGGCGGCGGCGATCCGCGGGGTGACCTTCCGCTG 120
QY 19 ----- 19
Db 121 CTCTTCAGAGAGAGAGACTCTCTTCTCACTGCGCTTGTAGCTGCGGGGTCTCTGG 180
QY 19 ----- 19
Db 191 AAGGTGCTGTGCTGCGGCGGTGGAGAGAGACTTGTGCTCTCTGCGGAACAGAGTG 240
QY 20 -----AlaGlnProGluGluLeuGlnIleProGluAspIleGluGlnThrAla 36
Db 241 GAAACTCAGAGAGAACTGAGAAATCTCAGATACCTGATGATATATATAGTAAACCTTT 300
QY 37 GUAValAsnMetThrGlyGlyThrAlaGluValLeuGluSerGluProThrGlnGly 56
Db 301 GAGAGAGAGAGAGAGAGATTCACAGCTGGCAGAAAGCAAGCATTAAGAGATTCAGAG 360
QY 57 ILeValGluThrIleThrAspGlyValThrIleGlyValIleGluLeuValIleGlu 76
Db 361 ATTGAGGAAATATGATGATGAGGCTGTGATCAAGATGCTGATGAACCAACTGTGAGAGAT 420
QY 77 LysProIleValValProIleProGlyAspGlyGlnIleValIleValIleValIle 96
Db 421 AAACCAAGGATATCCACCAAGAGAGATGGGCAAGATATATCAAAATTGACCAATG 480
QY 97 LeuIleValAspPheArgSerHisLeuAspIleValIleValIleValIleValIle 107

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Db 481 CTGAGAGAGATTTGGAAACCATCTTGACTACCGCAAAATTAATTCGATATCGGCTTT 540
QY 108 -----TyrSerGluTyrArgGlyIleArgAlaIle 117
Db 541 TGTGGGAAACCTACTCTGTAACTTGATATATCTTT-TTGGTAAATTAATTAAGTCGA 599
QY 118 Ile-----AspGlnHisGluGlyIle 124
Db 600 TTACTACAGAAATGCTCAATATTTACTTGATATCAAAATGATCAAACTCAATATCAT 659
QY 125 LeuGluAlaPheSerArgGlyTyrGluValLeuGlyPheThrArgSerAlaGluGlyIle 144
Db 660 TATTCGCTCTTCC-----AGCGTGAAGGCATT 689
QY 145 ThrTyrArgGlu-TTPAlaProGlyAlaHisSerAlaAlaLeuValIleAspPheAsnAs 164
Db 690 ACCTACCGAGAAATGGGCACCTGGAGACAGCTTCGACAGATTAGTGGTGAAGCTTCAAGA 749
QY 164 nTPAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTPGluIlePheIle 184
Db 750 TTGGAAACCAATGCAATACTATGACCAAGAAATGAGATGTGTTGGAGATTTCCT 809
QY 184 uProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIleArgGly 204
Db 810 GCCTTAACATGCTGATGATGCCCTGCTATTCCTCATGCTCAGTGAAGATTGCGAT 869
QY 204 LAspThrProSerGlyValIleAspSerIleSerAlaThrIleLysPheSerValGlnAla 224
Db 870 GATATCACCATCTGGCGCTAAAGATTCAATTCGCTGATTAAGTTGCTGTCCAGGC 929
QY 224 aProGlyGluIleProPheAsnGlyIle-----TyrTyrAspProProGlu 239
Db 930 TCCAGGTAATATACCGTAAACAGGATA-TTCCATTTTAACCTTATTTTCCATTCCTTA 988
QY 239 u-----GluIleValTyrValPheGlnHisPro-GlnProIleArgP 253
Db 989 TGTTGTTATACGCACTGACGAAATAATATGATTTCCACATCCTTCAACCTTAACGAC 1048
QY 253 roGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProIleAla 273
Db 1049 CAATATGCTGGCGATATATGAATCAATATTTGATATAGTACCCGGAACCGAAGATTA 1108
QY 273 snSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsn 293
Db 1109 ACACATATGCTAATTTTGGATAGGTGCTACCAAGAAATTAAGCTGTGGTATCAATG 1168
QY 293 lValGlnIleMetAlaIleGlnIleHisSerTyrTyrAlaSerPheGlyTyrHisValT 313
Db 1169 CTGTACAGATATATGCAATCCAGAGACCTCTTATTAAGCAAGCTTTGGTATCATGTA 1228
QY 313 hPheAsnPheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIleA 333
Db 1229 CTAACTCTTTGCGCAAGTACCGCTTTCGGAACCCAGAAAGCTTAAGATCTGATTTG 1288
QY 333 sPAsnAlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSerA 353
Db 1289 ATTAAGCTCAGAGCTTGTTGCTGTGATCTATATGATATGTTTCAAGTCAATGATCA 1348
QY 353 snAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGlyG 373
Db 1349 ACATATCCCTGATGATTTGATGTTGATGATGATCAATCAATTAATTCACAGAGTG 1408
QY 373 LysProArgGlyHisHisIleThrMetTrpAspSerArgLeuPheAsnTyrGlySerTrpGlu 393
Db 1409 GACCACGGGGTCACTACGAGATGGAGATCTCCGCTGTTCAACTATGGGAATGGGAAG 1468
QY 393 alleuArgPheLeuLeuSerAsnAlaArgTTPTrpLeuGluGluTyrLysPheAspGlyP 413
Db 1469 TTTTAAGTATTTATCTGATGATGCAATGCAAGTGGTCTGAACAAATTAAGTATGAGGT 1528
QY 413 hPheArgPheAspGlyValThrSerMetTyrThrHisHisGlyLeuGlnMetThrPheT 433

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Db 1529 TTCGATTGATGGGTGACCTCCATGATGTAATCTCATCTCATGTTTACAGGTGGCATTTA 1588
 QY 433 hgclyAsnTyrglyguTyrgPheglyPheAlaThrAspValaAspAlaValaValaTyrlu 453
 Db 1589 CTGGCAACTATGGCGAATATTTTGGATTGCTCTACTGATGTTGATGCGATGCTTACTTGA 1648
 QY 453 eclyeuValasnAspleuIleHISglyLeuHISProAspAlaValaSerIleGlyguAspv 473
 Db 1649 TGCTGCTGAACGATCTAATTCATGAGCTTATCTCTGAGCTGTAGCCATGCTGTAAGATG 1708
 QY 473 aISerGlyMetProThrPheCysIleProValaProAspGlyValaGlyPheAspTyra 493
 Db 1709 TCAGCGGAGATGCCACATTTTGTATTCCTGTCAAGATGGTGGTGTGTGTGACTATC 1768
 QY 493 rglLeuHISMetAlaValaAlaAspLysTrpIleGluLeuLeuLysGlnSerAspGluSer 513
 Db 1769 GTTTGATATGGCTGTACCGGACAAATGATCGAATCTCTCAAGCAAAAGTACAAATATT 1828
 QY 513 rPLysMetGlyAspIleValaHISThrLeuThrAsnArgArgTrpLeuGluLysCysValT 533
 Db 1829 GGAATAATGGGTGATATCGTGACACCCCTAAGATAGAGTGGTGCAGAGAAGTGTGTTA 1888
 QY 533 hTTrAlaGluSerHISAspGlnAlaLeuValGlyAspLysTrpIleAlaPheTrpLeu 553
 Db 1889 CTTATGCAAGAAAGTCATGACCAAGCACTAGTGTGTGCAAGACTATTGCAATCTGTGTTGA 1948
 QY 553 eUAspLys----- 555
 Db 1949 TGGATAGGTAAATCATTGTAGTTCACAAATCCAGGATATCTCAATCTCTTCAATGC 2008
 QY 556 --AspMetTyraSPheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyT 575
 Db 2009 AGGATATGATGATTTTATGCTGCTAGACAGACCTTCAACACTCGCATGATGCTGGA 2068
 QY 575 leAlaLeuHISLysMetIleHISLeuValThMetGlyLeuGlyGlyGlyTyrlu 595
 Db 2069 TAGCATTAATATAAAGATTAGGCTTGTGACCAATGGCTTAGAGAGGAGGCTATCTTA 2128
 QY 595 snPheMetGlyAsnGluPheGlyHISProGluTrpIleAspPheProArgGlyProGlnT 615
 Db 2129 ATTTCAATGGGAATGATGTTGGGCACTCTGATGATGATGATGATGATGATGATGATG 2188
 QY 615 hLeuProThrGlyLysValaLeuProGlyAsnAsnAsnSerTyraAspLysCysArgArg 635
 Db 2189 GCTTCCCAATGGCTGCTGCTCTCCAGAAACAATACAGATTGTATTAATGCGCTGTA 2248
 QY 635 rGPheAspLeuGlyAspAlaAspPheLeuArgTyrlsGlyMetGlnGluPheAspGln 655
 Db 2249 GATTTCACCTTGGAGATGACGATTATCTTAGATATCATGATGATGATGATGATGATG 2308
 QY 655 lAmetGlnHISLeuGluGluLysTyrglyPheMetTrpSerGlnHISGlnTyraValser 675
 Db 2309 CCAATGACGATCTTGAGGAAATAATGATTCATGACATCTGAGCACCAATATATATGCG 2368
 QY 675 rglLysHISGluGluAspLysValaIleIlePheGluArgGlyAspLeuValPheValPhe 695
 Db 2369 GGAACACAGAGAGGATTAAGTATCATCTTCAGAGAGAGATTTGTTGTTGCTGTTCA 2428
 QY 695 snPheHISTrpSerAsnSerPhePheAspTyraArgValaGlyCysSerArgProGlyLysT 715
 Db 2429 ACTTCACACGAGTAAATACATTTTTCATTCGCGCTTATTAACCTCGGAAGT 2488
 QY 715 yLysValaAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHIS 735
 Db 2489 ACAAGATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2548
 QY 735 spValaAspTyrgPheTrpHISGluHISProHISAspAsnArgProArgSerPheSerValT 755
 Db 2549 ATGCTGAGACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2608
 QY 755 yTThrProSerArgThrAlaValaValaValaValaValaValaValaValaValaVal 768

RESULT 10
 AAV38720
 ID AAV38720 standard; DNA; 3090 BP.
 XX
 AC AAV38720;
 XX
 DT 21-SEP-1998 (first entry)
 XX
 DE Full length cassava tuber cDNA in pS1146.
 XX
 KM Starch branching enzyme; SBE; cassava; ss.
 XX
 OS Manihot esculenta.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 35..2760
 FT /*tag= a
 FT /note= "these nucleotides are SBE II sequence, the
 FT remainder are derived from the plasmid"
 FT /*tag= b
 FT /product= "SBE II"
 XX
 PN W09820145-A2.
 XX
 PD 14-MAY-1998.
 XX
 PR 04-NOV-1997; 97WO-GB003032.
 XX
 PR 05-NOV-1996; 96GB-00023095.
 XX
 PA (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX
 PI Jobling SA, Safford R;
 XX
 DR WPI; 1998-286958/25.
 DR P-PSDB; AAM62600.
 XX
 PT Starch branching gene from cassava - useful for producing altered plants
 PT giving modified starch.
 XX
 PS Claim 2; Fig 13; 67pp; English.
 XX
 SS The present sequence encodes starch branching enzyme (SBE) II. It was
 CC isolated from cassava tubers. The products can be used for producing
 CC plants having altered starch quantities and qualities. They can also be
 CC used for producing altered plants such as cassava, banana, potato, pea,
 CC tomato, maize, wheat, barley, oat, sweet potato and rice plants
 XX
 SQ Sequence 3090 BP; 877 A; 578 C; 721 G; 914 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5.4e-302 Length: 3090
 Score: 3292.00 Matches: 595
 Percent Similarity: 86.49% Conservative: 71
 Best Local Similarity: 77.27% Mismatches: 72
 Query Match: 78.96% Indels: 32
 DB: Gaps: 4
 US-09-508-377-12 (1-768) x AAV38720 (1-3090)
 QY 23 GlnGluLeuGlnIleProGluAsp-----IleGluGlnThrAlaGluVal 38
 Db 332 GAGAAAGGCTCTTGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 391
 QY 39 AsnMetThrGly-----GlyThrAlaGluLysLeu--- 48
 Db 392 GAACCACTGCGACAGATTGTGGAGGATCCAGTTCTTGTGATGACAGAGAGTCTTG 451
 QY 49 -----GluSerSerGluProThrGlnGlyIleVal 58

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QY 59 GIUThrlleThraSpGlyValThrlySGlyVallySGlyLeuValValGlyGlyPro 78
DB 512 GAGACAAATTAGCATGGAAAAAGTGA-----TCTAAACA 547
QY 79 ArgValValProlyProGlyAspGlyGlyIleTyrglyIleAspProThrLeuLys 98
DB 548 AGGTCATCTCTCCACCTCGCAGTGGGCGAGAAATATGACATGATCCAGCTTGGCA 607
QY 99 AspPheAspSerHisLeuAspTyrArgTyrSerGlyTyrArgArgIleArgAlaIle 118
DB 608 GGTTTCCCGACACCTTGACTACCATCTTCACAGTACMAAAGCTGCGAGGAAATT 667
QY 119 AspGlnHisGlyGlyGlyLeuGlyAlaPheSerArgGlyTyrGlyLeuGlyPheThr 138
DB 668 GACAAGTATGAAGGCTGGTGGATGCTCTCTCGGATTTGAAAAGTTGGTTCTTA 727
QY 139 ArgSerAlaGlyGlyIleThrTyrArgGlyTyrAlaProGlyAlaHisSerAlaIleu 158
DB 728 CGCACTGAAACAGGAAATACCTATAGGGATGGGCACTGAGCTACGCGCTGCACTT 787
QY 159 ValGlyAspPheAspThrAspProAspAlaAspThrMetThrArgAspAspTyrGly 178
DB 788 ATGGAGATTTACAAATGGAACTCTAATGCAAGATGTCATGACCTCGGATAGTTGGT 847
QY 179 ValTyrGlyIlePheLeuProAspAlaAspGlySerProAlaIleProHisGlySer 198
DB 848 GTCTGGAGATTTTGGCAATATACGAGATGGTTCCACCAATCTCTGATGTTT 907
QY 199 ArgValIleValIleArgMetAspThrProSerGlyValIleAspSerIleSerAlaTyr 218
DB 908 CGAGTAAAGATCGCATGATGATCTCCATCTGCACTCAAAAGATTCAATCTCTGGATC 967
QY 219 LysPheSerValGlnAlaProGlyGlyIleProPheAspGlyIleTyrTyrAspProPro 238
DB 968 AAGTTCTAGTTCAAGCACCCTGATGATATCCATACATGCAATACATCTATGATCCCA 1027
QY 239 GlnGlyGlyTyrValIlePheGlnHisProGlyIleProLysArgProGlySerLeuArgIle 258
DB 1028 AAGGAGGAGAGTATGTGTTCAACATCTCTCAGCAAAAGACCAAAATCACTTAGATT 1087
QY 259 TyrGlySerHisIleGlyMetSerSerProGlyIleProLysIleAspSerTyrAlaPhe 278
DB 1088 TATGATCTCATGTGGGATGATGATGATGAGCCAAATATTAACATATCCCACTT 1147
QY 279 ArgAspGlyValLeuProArgIleLysArgLeuGlyIleTyrAspAlaValGlnIleMetAla 298
DB 1148 AGAGATGATATCTCTCTCGCATCAAAAAGCTTGGCTCAATGCTGTCAGATCAGGTT 1207
QY 299 IleGlnGlnHisSerTyrTyrAlaSerPheGlyIleHisValThrAspPhePheAlaPro 318
DB 1208 ATTCAGAGCAATTCCTATATATCTGATTTGGGACCAATGTCACAAACTTTTTCACCT 1267
QY 319 SerSerArgPheGlyThrProGlyAspLeuLysSerLeuIleAspArgAlaHisGlyLeu 338
DB 1268 AGCAGCCGATTTGGACATCTCGATGATTTGAAGTCTTTATATGATTAAGCTCATAGTTA 1327
QY 339 GlyLeuLeuValLeuMetAspIleValHisSerHisSerSerAspAspThrLeuAspGly 358
DB 1328 GGGCTGCTGTGTTCTCATGATTTGTTCTATGCCATGCGTCAAAATATACCTTGGATGGG 1387
QY 359 LeuAspGlyPheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisHis 378
DB 1388 CTGAACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1447
QY 379 TyrMetTyrAspSerArgLeuPheAspThrArgIleTyrGlyValIleuArgPheLeu 398
DB 1448 TGGTTGTGGGACTCTCGCTTTTCAACTATGAGAACCTGGGAGGTCTTAAGATTCTTCTT 1507
QY 399 SerAspAlaArgTyrTyrLeuGlyIleTyrLysPheAspGlyPheArgPheAspGlyVal 418
DB 1507
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QY 419 ThrSerMetTyrThrHisIleGlyLeuGlnMetThrPheThrGlyAspTyrGlyGlu 438
DB 1568 ACTCCATGATATGATACCTCCCATGGTGGTGGAGTCTTTTACCTGGCACTCAATGAG 1627
QY 439 TyrPheGlyPheAlaThrAspValAspAlaValIleTyrLeuMetLeuValAspLeu 458
DB 1628 TACTTGGATGATGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1687
QY 459 IleHisGlyLeuHisProAspAlaValSerIleGlyGlyAspValSerGlyMetProThr 478
DB 1688 ATTCACGGCTCTTCCCTGAGGCTGTTCATTTGGTGAAGATGTTAGCGGAAAGCCAAACA 1747
QY 479 PheCysIleProValProAspGlyGlyValGlyPheAspTyrArgLeuHisMetAlaVal 498
DB 1748 TTTTGCATTTCCAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1807
QY 499 AlaAspLysTyrIleGlyLeuLeuLysGlnSerAspGlySerTyrLysMetGlyAspIle 518
DB 1808 GCCGATTAATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1867
QY 519 ValHisThrLeuThrAspArgArgTyrLeuGlyLysCysValThrTyrAlaGlySerHis 538
DB 1868 GTGATACCTACCAACAGAGGTTGGTGGAAATGTGTGCTTATGCTGATGATGATGATGATG 1927
QY 539 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTyrLeuMetAspLysAspMetTyr 558
DB 1928 GACCAAGCTCTGTTGGTGGACAAAACATATGATGATGATGATGATGATGATGATGATGATG 1987
QY 559 AspPheMetAlaLeuAspArgProSerThrProGlyIleAspArgGlyIleAlaLeuHis 578
DB 1988 GACTTCATGCGCTCGTGAACAGACATCTCTCTTATAGATCGTGAATATACATGTCAC 2047
QY 579 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyGlyIleTyrLeuAspPheMetGly 598
DB 2048 AAAATGATCAGCTTATTCATCCATGGGCTTGGCGGAGAAAGATATTTGAATTTTAGGA 2107
QY 599 AsnGlyPheGlyHisProGlyIleAspPheProArgGlyProGlnThrLeuProThr 618
DB 2108 AATGATTTTGGACATCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2167
QY 619 GlyLysValLeuProGlyAspAspAspSerTyrAspLysCysArgArgPheAspLeu 638
DB 2168 GGTAAAGTATTCAGGAGAACCAACACAGTTATGATTAATGCGTCGTGATGATGATGATG 2227
QY 639 GlyAspAlaAspPheLeuArgTyrHisGlyMetGlnGlyPheAspGlnAlaMetGlnHis 658
DB 2228 GGTATGACAGATATCTATGATATATCATGAATGCAAGATTTGATCAGCATGCAACAT 2287
QY 659 LeuGlyGlyLysTyrGlyPheMetThrSerGlyHisGlyIleValSerArgGlyHisGly 678
DB 2288 CTGGAAGAGCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2347
QY 679 GlnAspLysValIleIlePheGlyGlyArgIleAspLeuValPheValPheAspPheHisTyr 698
DB 2348 GGAATGCGATCATGTTGCTTTGAGAGGGGAAACCTGTTTGTATTCACATTTCACTTGG 2407
QY 699 SerAspSerPhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAla 718
DB 2408 ACTACACACTTTCAGATTTACGAGATGCTGCTTCAAGTCAAGAAAGTAAAGATGTTGT 2467
QY 719 LeuAspSerAspAspAlaLeuPheGlyGlyIlePheSerArgLeuAspHisAspValAspTyr 738
DB 2468 TTGATCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2527
QY 739 PheThrThrGlnHisProHisAspAspAlaArgProArgSerPheSerValTyrThrProSer 758
DB 2528 TTCACTTTCAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2587
QY 759 ArgThrAlaValIleTyrAlaLeuThrGlu 768
DB 2588 AGGACAGAGTGTCTATGCTTTAGTGA 2617
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Db 1378 CATCATGAGCTCTGCTGGATTGATTTACTGGAACTACACCGAATCTTGGATTGGAAACT 1437
QY 445 ASPVALASPAVALAVALTYRLEUWETLEUVALASAPLEU1LHISGLYLEUHIISPRO 464
Db 1438 GATGTGGATGTGCGAATTAATCTCATCTGCTGTTATGATATGATCATGGCTTACCT 1497
QY 465 ASPALAVASER1LEGLYGLUASPAVALSERGLYMETPROTHRPHCYGLLEPROVALPRO 484
Db 1498 GAAGCGATTACCGTGTGGAAGATGTGTATGATGCCAACAATCTGTATCTCTGCCAA 1557
QY 485 ASPGLYGLYVALGLYPHASPRTYRARGLEUHIISMETALAVALLASAPLYSTRP1LEGLU 504
Db 1558 GATGGGCGCTGGATTGACTTACCTTACATGCGCATAGCTGATAGAGGATAGAA 1617
QY 505 LEUWETLYGINSERASPSGLUSERTRYPLYSMETGLYASPILEVALHISTHLEUTHRAEN 524
Db 1618 ATGCTCAAGAAAGAGATGAAGACTGGCAAAATGGCGCATCATTTACACACTTACCAAC 1677
QY 525 ARGARGTTPLEUGLULYCYCYVALTHRTYRAG1USERHISASPIALAVALLAUVALGLY 544
Db 1678 AGAAGGTGTGAGAAAGTGTATCTTATGCTGAAGTCAAGATCAAGCTCTTGTTGAT 1737
QY 545 ASPLYSTR1LEALPHETRYLEUWETASPLYASAPMETTYRASPHEMETALALEUASP 564
Db 1738 GATMAAACAAATTCCTTCTGTTATGACAAAGATATGTATGATTTCAATGGCAGTAAAC 1797
QY 565 ARGPROSETHRPROARG1LEASPARGLYLEALALEUHIISLYSMET1LEARGLEUVAL 584
Db 1798 AGACCATCAACTCCCTTATCATATGAGGAATAGCTTSCACAAATGATAGGCTTATA 1857
QY 585 THMETGLYLEUGLYGLYGLULYTYRLEUASPMHMETGLYASGLUHEGLYHISPRO 604
Db 1858 ACTATGGGATTAGGGGAGTGAAGGTACTTAATTTATGGAAACCAATTCGGACATCCA 1917
QY 605 GLUTRPILEASPPHAPROARG1LYPROGINTHRLEUPROTHRG1LYLYSVALLEUPROGLY 624
Db 1918 GAAATGGATGATTTTCCAGAGCGCAGCAGCGCTTTCGATGGTACGCTGATCTCTGGC 1977
QY 625 ASNSASNASERTYRASP1LYSCYARGARGARGPHEASPLEUGLYASPA1AASPHELEU 644
Db 1978 AACAAATTCAGTATGACAAATGCGCGCCAGATTGATCTTGGGATGACAGATTATCTC 2037
QY 645 ARGTYRHSGLYMETGLINLUPHEASPG1NALAMETGLHISLEUGLULYLYSTYRGLY 664
Db 2038 AGATACCGCGGACTCAAAATTTGATGACGCAATGCCAATCTTGAAGGAATTCGGGT 2097
QY 665 PHEMETRUSERG1LHISGLINTYRVALSERARGLYSHISGLULUASPLYVAL1LE1LE 684
Db 2098 TTTATGACTTCGAGAGCACCAATTCATATCAAGAAAAGACGAAGCAGATAGATGCTA 2157
QY 685 PHEGLUARG1LYASPLEUVALPHEVALPHEASPMHIS1ETRYSERASNSERPHIEPHEASP 704
Db 2158 TTGAAAAGAGGATCTGCTCTTGTGCTTAACTTCACTGACGACGACGACGACTTTGAT 2217
QY 705 TYRARGVALGLYCYSERARGPROGLYLYSTYRLYSVALALEUASPMSEPARAPASALA 724
Db 2218 TAACCCATGATGTGCTCCAAAGCTGGAATAATTAATGCTATTTGGCTGAGCAGATCT 2277
QY 725 LEUPHEGLYGLYPHESERARGLEUASPHISASPVASPLYRPHETHRTHRG1LHISPRO 744
Db 2278 CTCCTTTGGGATTCATATAGCTCGATCGAAGCAGAGACTTCACTTATGATGGCTTA 2337
QY 745 HISASPMASPARPROARGSERPHESERVALTYRTHPROSERARGTHRALAVALLAVALTYR 764
Db 2338 TACGACGAACGACCGCTGCTCTTCATGAGTGTATGACACCGGTGAAACCGCGTGTAT 2397
QY 765 ALALEU 766
Db 2398 GCTTTA 2403

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RESULT 12
ADA68438
ID ADA68438 standard; DNA; 2418 BP.

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XX AC ADA68438;
XX AC
XX 20-NOV-2003 (first entry)
XX DE Arabidopsis thaliana gene, SEQ ID 672.
XX DE
XX KW Plant; bacterial infection; fungal infection; viral infection; ds.
XX OS Arabidopsis thaliana.
XX PN W02003000898-A1.
XX PD 03-JAN-2003.
XX PF 22-JUN-2001, 2001MO-IB001105.
XX PR 22-JUN-2001, 2001MO-IB001105.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,
XX PI Katagiri F, Qian S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
XX DR WPI, 2003-175290/17.
XX PT Identifying at least one gene involved in plant resistance or response to
XX PT pathogenic infection for conferring resistance or tolerance to a plant to
XX PT bacterial, fungal or viral infection by determining or detecting plant
XX PT gene expression.
XX PS Claim 6; SEQ ID NO 672; 899bp; English.
XX CC The present invention relates to a method (M1) for identifying genes
XX CC involved in plant resistance or response to pathogenic infection. M1
XX CC comprises identifying a gene whose expression is significantly altered in
XX CC the incompatible interaction of plant gene expression relative to
XX CC expression of the gene in an uninfected plant, in a mutant plant that
XX CC does not express a gene associated with response to pathogenic infection,
XX CC or in a corresponding incompatible or compatible interaction. (M1) is
XX CC useful for conferring resistance to resistance or tolerance to a plant to
XX CC bacterial, fungal or viral infection. The present sequence was used to
XX CC illustrate the invention.
XX SQ Sequence 2418 BP; 692 A; 482 C; 556 G; 688 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,46e-299 Length: 2418
Score: 3258.00 Matches: 584
Percent Similarity: 86.48% Conserved: 75
Best Local Similarity: 76.64% Mismatches: 71
Query Match: 78.15% Indels: 32
DB: 7 Gaps: 4

US-09-508-377-12 (1-768) x ADA68438 (1-2418)
QY 18 ALAALALAGLNPORG1LUGLULUENGL1LEPROGU----- 29
Db 175 GCATCTCTGCTCTGAGAAAGTCTTACTGATATCTTGTATGATGATGCCAGAGT 234
QY 30 -----ASPILEGLULUGLINTHRALAG1UVALASPMETHRGLYTHR 44
Db 235 TTTTCAAGATATTGATCTGAAAGTCAACCAATGCAATGAT----- 276
QY 45 ALAG1ULYSLUG1USERSEGLUPROTHRG1NGLYLEVALGLUTHR1LETHRASPGLY 64
Db 277 ACTAGGCGAGTAAAGACGAAGACCAACCAATGAAGCTT----- 315
QY 65 VALTHR1YSG1LYVALYGLUENVALVALGLYGLULYSPROARGVALVALPROLYSPRO 84
Db 316 -----GTCAGAGAGAGA-----GGGTGAAACCAAGAAATGTTCCCAACCG 357
QY 85 GLYASPG1LYGLULYSL1ETRYGLUL1LEASPMHLEUWETLYSASPMHETR1LEU 104

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XX DE Full length cassava tuber cDNA in pSJ107.
 XX Starch branching enzyme; SBE; cassava; ss.
 XX Manihot esculenta.
 XX OS
 XX Key Location/Qualifiers
 XX FT CDS 21..2531
 XX FT /*tag= a
 XX FT /product= "SBE II"
 PN W09820145-A2.
 PD 14-MAY-1998.
 PF 04-NOV-1997; 97WO-GB003032.
 PR 05-NOV-1996; 96GB-00023095.
 PA (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 PI Jobling SA, Safford R;
 XX WPI; 1998-286958/25.
 DR P-PSDB; AAW62599.
 XX Search branching gene from cassava - useful for producing altered plants
 XX PT giving modified starch.
 XX PS Claim 2; Fig 4; 67pp; English.
 CC The present sequence encodes starch branching enzyme (SBE) II. It was
 CC isolated from cassava tubers. The products can be used for producing
 CC plants having altered starch quantities and qualities. They can also be
 CC used for producing altered plants such as cassava, banana, potato, pea,
 CC tomato, maize, wheat, barley, oat, sweet potato and rice plants
 XX Sequence 2913 BP, 818 A, 549 C, 680 G, 866 T; 0 U; 0 Other:
 SQ
 Alignment Scores:
 Pred. No.: 3.09e-297 Length: 2913
 Score: 3241.50 Matches: 582
 Percent Similarity: 87.53% Conservative: 78
 Best Local Similarity: 77.19% Mismatches: 83
 Query Match: 77.75% Indels: 11
 Gaps: 2

QY 135 LeuGlyPheThrArgSerAlaGluGlyIleThrTyrArgGluTrpAlaProGlyValHis 154
 DB 591 TTGGTCTTCACGACGATGAAACAGAAATACCTTATAGAGAGTGGGACAGAGCTACG 650
 QY 155 SerAlaAlaLeuValGlyAspPheAsnAspTrpAsnProAsnAlaAspTrpMetThrArg 174
 DB 651 TGGGCGCATGGATGGAGATTTCATTAACCTGAATCCATATGACATGTCATACGACG 710
 QY 175 AspAspTyrGlyValTrpGluIlePheLeuProAsnAlaAspGlySerProAlaIle 194
 DB 711 AATGAGTGTGTGTCTGGAGATCTTTTCCGAATTAATGACATGGTTCCACCAAT 770
 QY 195 ProHisGlySerArgValIleArgMetAspThrProSerGlyValIleAspSerIle 214
 DB 771 CCCCATGGTCTCGAGTAAAGATACGATGATATCTCATCTGGCAACAAAGATTCTATT 830
 QY 215 SerAlaTrpIleLysPheSerValGlnAlaProGlyGluIleProPheAsnGlyIleTyr 234
 DB 831 CCTGCTGGATCAAGTTCTCATGATCAAGCACAGTGAACCTCCATATTAATGGCATATAC 890
 QY 235 TyrAspProProGluGluGlyTyrValPheGlnHisProGlnProLysArgProGlu 254
 DB 891 TATGATCTCCCGAGAGAGAAAGTATGTGTTCAAAATCCTCAGCCAAAGACAAAA 950
 QY 255 SerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSer 274
 DB 951 TCACCTCGGATTTATGATGCGACAGTGAATGATGATGACGACAGATATTAAACACA 1010
 QY 275 TyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsnAlaVal 294
 DB 1011 TATGCCAAGCTTATAGATGATGTGTCTTCGATCAAAAGCTTGGCTACAAAGCTCTT 1070
 QY 295 GlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsn 314
 DB 1071 CAGCTATGCTATTTCAGAGCATTCATATTATGCTATGTTGGATACAGTCAAC 1130
 QY 315 PhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIleAspArg 334
 DB 1131 TTTTATGACACTGACAGCCGATTTGGAATCTCGATGATTTAAAGTCTCTATATATATAA 1190
 QY 335 AlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSerAsn 354
 DB 1191 GCTCAGCAGTTAGATCTTCTGTCTCATGATATGTTGTCATAGCAGTCAACTAT 1250
 QY 355 ThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGlyPro 374
 DB 1251 ACGTTGATGCGCTGAATATGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1310
 QY 375 ArgGlyHisIleTrpMetTrpAspSerArgLeuPheAsnTyrGlySerTrpGluValLeu 394
 DB 1311 CGGGGTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1370
 QY 395 ArgPheLeuLeuSerAsnAlaArgTrpTrpLeuGluGluTyrLysPheAspGlyPheArg 414
 DB 1371 AGTTTCTTCTTCAATGACAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1430
 QY 415 PheAspGlyValThrSerMetMetTyrThrHisIleGlyLeuGlnMetThrPheThrGly 434
 DB 1431 TTGATGGGGGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1490
 QY 435 AsnTyrGlyGluTyrPheGlyPheAlaThrAspValAspAlaValValTyrLeuMetLeu 454
 DB 1491 AACTACATGAATACCTTGGATATGACAACTATGATGATGATGATGATGATGATGATGAT 1550
 QY 455 ValAsnProLeuIleHisGlyLeuHisIleProAsnAlaValSerIleGlyGluSerValSer 474
 DB 1551 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1610
 QY 475 GlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyrArgLeu 494
 DB 1611 GGATGCCAACAGTTTGATTCGGGTTGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1670

QY 495 HisMetAlaValAlaAspIleuTrpIleGluLeuLeuGlnSerAspGluSerTrpIle 514
 Db 1671 CACATGGCGTGTGGCATTAAGGCTTGAGATTATTCAGAAAGAGATGAAGATTGGAAA 1730
 QY 515 MetGlyAspIleValHisThrLeuThrAsnArgArgTrpLeuGlnIleValThrTyr 534
 Db 1731 ATGGGTGACATTGTACATATGCTGACCAACAGCGGTGGTGAAGAGTCTGTTCTAT 1790
 QY 535 AlaGluSerHisAspGlnAlaLeuValGlyAspIleThrIleAlaPheTrpLeuMetAsp 554
 Db 1791 GGTGAAGTCATGACACAGCGCCCTGTGGTGAACAAATCATTCATTGGCTGATGGAC 1850
 QY 555 LysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAspArgGly 574
 Db 1851 AAGGATATGATGACTTCATGGCTCTTGACAGACCATCTACTCTCATAGATCGTGA 1910
 QY 575 IleAlaLeuHisGlyMetIleArgLeuValThrMetGlyLeuGlyGluGlyTyrLeu 594
 Db 1911 GTAGCATTCGCAAAATGATCAGGCTTATTCATGAGGATTAAGCGGAGAGATATTG 1970
 QY 595 AsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGlyProGln 614
 Db 1971 AATTTTAAAGGAAATGAATTTGGACACCCGAGTGATTTTCCAAAGAGTGATCTA 2030
 QY 615 ThrLeuProThrGlyLysValLeuProGlyAsnAsnSerTyrAspIleCysArgArg 634
 Db 2031 CATCTTCCAGTCGTGTAATTTGTTCTCGGGAACAATTACGTTATGTAATATCGCGCGT 2090
 QY 635 ArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnIlePheAspGln 654
 Db 2091 AGGTTTGAATCTAGGCAATTCAAAGCATCTGAGATATCATGAAATGCAAGTTGATCA 2150
 QY 655 AlaMetGlnHisLeuGluGluIleuTyrGlyPheMetThrSerGlnHisGlnIleValSer 674
 Db 2151 GCAATTCAGCATCTTGAAGAGCCTATGTTTCATGACTTCTGAGCACCATACATATCA 2210
 QY 675 ArgGlyHisGluGluAspLysValIleIlePheGluArgGlyAspLeuValPheValPhe 694
 Db 2211 CGGAAGGATGAAGAGATCGATCATGTCTCTGAGAGGGGAAACCTCGTTTGTGATTC 2270
 QY 695 AsnPheHisTrpSerAsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLys 714
 Db 2271 AATTTTCATTGGACTGACGACTATCGSATTACCGAGTTGGCTTAAAGCCAGAAAG 2330
 QY 715 TyrLysValAlaLeuAspSerAspAlaLeuPheGlyGlyPheSerArgLeuAspHis 734
 Db 2331 TACAGATAGTCTTGATTCAGATGATCCCTTTGAGAGGCTTTGGCAGGCTTAGTCAT 2390
 QY 735 AspValAspTyrPheThrThrGluHisProHisAspAsnArgProArgSerPheSerVal 754
 Db 2391 GATGACAGACACTTCAGCTTGAAGGCTGTGAGATTAACGGGCTCGATCCTTCATGCTG 2450
 QY 755 TyrThrProSerArgThrAlaValAlaTyrAlaLeuThrGlu 768
 Db 2451 TACACCATCTGTAACAGCAGTGTCTATGCTTATGATGAG 2492
 RESULT 14
 ID AAT17267 standard; DNA; 2531 BP.
 XX AAT17267;
 XX
 DT 03-MAR-1997 (first entry)
 XX
 DE Class A starch branching enzyme (direct sequencing).
 XX
 KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
 XX amylose; viscosity; potato; ss.
 OS Solanum tuberosum.
 XX
 XX
 XX W09634968-42.
 XX

PD 07-NOV-1996.
 XX
 PF 03-MAY-1996; 96WO-GB001075.
 XX
 PR 05-MAY-1995; 95GB-00009229.
 PR 10-APR-1996; 96GB-00007409.
 XX
 PA (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX
 PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R.
 PI Sidebottom CM, Westcott RJ.
 XX
 DR WPI: 1996-506170/50.
 DR P-PSDB: AAR93804.
 XX
 PT New potato plant starch having high amylose content - also class A starch
 PT branching enzyme and corresp. DNA to alter the viscosity of starch; for
 PT use in food, biodegradable products, adhesives, etc.
 XX
 PS Example 1; Fig 9; 142pp; English.
 XX
 CC Class A starch branching enzyme (SBE) has been obtained from potatoes. In
 CC class A SBE mols., a flexible N-terminal domain, is found, which is not
 CC found in class B mols. This sequence was obtained by direct sequencing of
 CC PCR fragments amplified from first strand cDNA. Nucleotides which could
 CC not be unambiguously assigned are indicated using standard IUPAC notation
 XX
 SQ Sequence 2531 BP; 735 A; 458 C; 599 G; 723 T; 0 U; 16 Other;
 Alignment Scores:
 Pred. No.: 4,266-293 Length: 2531
 Score: 3197.00 Matches: 586
 Percent Similarity: 82.53% Conservative: 80
 Best Local Similarity: 72.61% Mismatches: 93
 Query Match: 76.69% Indels: 48
 Gaps: 6
 US-09-508-377-12 (1-768) x AAT17267 (1-2531)
 QY 2 AlaThrPheAlaValSerGlyAlaThrIleu-----GlyValAlaArgProPheAla 19
 Db 92 TCTACAGTTGAGACATCGCGGAAAGTCTTGCTGCTGGAAYCAGAGTATAGCTCTCA 151
 QY 20 AlaGlnProGluGluLeuGlnIleProGlu----- 29
 Db 152 TCTTCAACAGACCAATTTGAGTCTCTGACATCTCCAGAAATTCCTCCAGCATCACT 211
 QY 30 AspIleGluGluGlnThrAlaGlu----- 37
 Db 212 GATGAGATGATGTCACAAATGAGACACGCTACGACATTAAACTGAGAACATGACGTT 271
 QY 38 -----ValAsnMetThrGlyGlyThrAlaGlu----- 46
 Db 272 GAGCGCTGAGAGATCTTACAGGAAGTGTGAAGAGCTGATTTGCTTCATGACATGAA 331
 QY 47 -----LysLeuGluSerSerGluProThrGlnGlyIleValGluThrIle 61
 Db 332 CTACAAAGAGTGTAACTGAGAGAGCTAAACATTAAATCTTCTGAAAGACAAATT 391
 QY 62 ThrAspGlyValThrLysGlyValLysGluLeuValAlaGlyLysProArgValVal 81
 Db 392 ATGATGATGATCGATAGG---ATCAGAGAG-----AGGGGCATC 427
 QY 82 ProLysProGlyAspGlyGlnLysIleTyrGluIleAspProThrIleuLysAspPheArg 101
 Db 428 CCTCCACCTGACCTTGCTGTCAGAAAGATTATGAAATGAGCCCTTTTGACAAACTATCGT 487
 QY 102 SerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAlaIleAspGlnHis 121
 Db 488 CAAACCTTGATTAACAGGATATTCACGATCAAGAACTGAGGAGGCAATGACAGTAT 547
 QY 122 GluGlyLysLeuGluAlaPheSerArgGlyTyrGluLysLeuGlyPheThrArgSerAla 141

Db 548 GAGGGGTGTTTGAAGCTTTTCTCGTGTTATGTAAGAAAAATGGGTTTCACGTAGTCT 607
 QY 142 GUGUUYLLETHRYTRAGGLUTPRALASPROGIALAHISERVALALEUVALGLYASP 161
 Db 608 ACAGGTTACCTTACCGGAGGAGGCTCTGGTCCGCTCAGCTGCCCCCTCATTTGGAGAT 667
 QY 162 PHEASANTTPASNPASNALASPTTHMETNTRARGASPDYRGILYALTRPGU 181
 Db 668 TTCAACAATTTGGACGCAATGCTGACATTAATGATCGGAATGAAATTTGGTCTGGGAG 727
 QY 182 ILEPHEUPROASNALASPDGLYSEPROAIIIEPROHISGLYSEARVALYS 201
 Db 728 ATTTTCTGCAAAATTAATGTGATGTTCTCTGCAATTTCCATGGGTCAGAGTGAAG 787
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 Db 788 ATACGATGACACTCCATCCAGGTGTAAAGATTCATTCCTGCTTGATCAACTACTCT 847
 QY 222 VALGINALAPROGLYGLULIETROPHASNGILYILEYTRYRASPPROBROGLUGLU 241
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 QY 262 HISTILEGLYMETSESERPROGLUPROLYSILEASNSERTYRVALASNPHEARGASPU 281
 Db 968 CATTTGAAATGAGTAGTCGAGCCTAAATTAATCTACGTGATTTAGAGATGA 1027
 QY 282 VALLEUPROARGILEYVARGPHEUGILYTRASNALAVALGINLEWECHALILEGINGLU 301
 Db 1028 GTTCTCTCCGCTAAAAAASCTTGGTACATGCGGTCAATTAATGCTATTCAGAG 1087
 QY 302 HISERTYTRYALASERPHUGILYTRYHISVALTHASNPHEALAPROSESERARG 321
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 Db 1148 TTGGAAAGCCCGACGACCTTAAGCTTTGATTAAGAAAGCTCATAGCTAGGAATGTT 1207
 QY 342 VALLEUMETASPILEVALHISSEHISSESERASNSNTHREUSAPGLYEUANGILY 361
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 QY 362 PHEASPGILYTHASPTTHHISITYRPHENISGLYGLYPROARGILYHISITRPMETTR 381
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 Db 1628 CCGCTTCAAGATGAGGAGTGTGGCTTGTGATATCGCTGATATGGAATTTGCGATGAA 1687

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 QY 562 ALALEUASPARPROSETHNPROARGILEASPARGLYILEALALEUHIISLYMETILE 581
 Db 1868 GCTCGATATGACCGTCAACATCATTAATGATGCTGGGATGATGATGACAGATGAT 1927
 QY 582 ARGLEUVALTHMETGLYLEUGILYGLYTRYTRYRLEUASNPHEMETGLYASNGILUPHE 601
 Db 1928 AGGCTTGATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1987
 QY 602 GLYHISPROGLUTRIPLEASNPHEARGILYPROGLNTHREUPROTHRGILYLYSVAL 621
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 Db 2048 ATTCGGGAACCAATTCAGTTATGATTAATGACAGAGAGATTTGACCTGGAGATGCA 2107
 QY 642 ASPHELEUARGTRYRHSISGLYMETGLINGLUPHEASPDNALAMETGLINILEUGILU 661
 Db 2108 GAATATTTAAGATACCAATGGGTGCAAGAAATTTGACGGGTATGACATATCTTGAAGAT 2167
 QY 662 LYSTYRGLYPMETTHNSEERGLIHISGLINTYRVALSERARGLSHISGLUGLUSPLYS 681
 Db 2168 AAATATAGTTTATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2227
 QY 682 VALILEPHEGLUARGILYASPLEUVALPHEVALPHEASNPHEHISTRSEHNSER 701
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 QY 702 PHEPHESPYTRYRGLYGLYCYSEERARGPROGLYLYSTYRILYVALALEUASPSER 721
 Db 2288 TATTCAGACTATGCAATGAGCTGCTGAAAGCTGAAATATCAAGTTGGCTTGACATCA 2347
 QY 722 ASPASPALALEUPHEGLYGLYPHESEARGLEUASPHISASPVASPTYRPHETHRTHR 741
 Db 2348 GATGATCCATTTTGGTGGCTTGCGGAGATGATGATGATGATGATGATGATGATGATGATG 2407
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 Db 2408 GAAGGATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2467
 QY 762 VALVALTYRVALALEUTHINGLU 786
 Db 2468 GTGCTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

RESULT 15

ABK50301
ID ABK50301 standard; cDNA; 2563 BP.

AC ABK50301;

DT 15-JUL-2002 (first entry)

DE Potato cDNA encoding starch branching enzyme, SBE II.

XX Potato; starch branching enzyme, SBE II; glucan branching enzyme; GBE;
 XX ss; gene; plant; transgenic; antisense; food industry; paper industry;
 XX chemical industry.

OS Solanum tuberosum.

XX

Key	Location/Qualifiers	3. .2552
FT CDS	/*tag= a	
FT	/product= "SBE II"	
FT	/partial	
FT	/note= "No start codon shown"	
XX		
PN	GB2360521-A.	
XX		
PD	26-SEP-2001.	
XX		
PF	20-MAR-2000; 2000GB-00006733.	
XX		
PR	20-MAR-2000; 2000GB-00006733.	
XX		
PA	(DANI-) DANISCO AS.	
XX		
PI	Poulsen P, Sorensen IS;	
XX		
DR	WPI: 2001-650142/75.	
XX		
DR	P-PSDB; ANU80169.	
XX		
PT	New transformed plants with reduced endogenous starch branching enzyme and heterologous glucan branching enzyme activities, useful for producing starch with improved properties, which is in the food, paper and chemical industries.	
XX		
PS	Example 1; Page 31-35; 61pp; English.	
XX		
CC	The invention relates to a transformed organism, preferably a transformed plant, having a reduced endogenous starch branching enzyme (SBE) activity, and having a heterologous glucan branching enzyme (GBE) activity. The reduced SBE activity is effected via expression of a nucleotide sequence that is antisense to at least part of a SBE exon. Also included are a method of producing starch with altered characteristics comprising (a) providing a plant having reduced endogenous SBE activity, and having heterologous GBE activity (b) propagating the plant of (a) and optionally (c) obtaining starch from the plant; starch obtainable from the transformed plant; and a nucleic acid construct system capable of directing the expression of all or part of one or more antisense SBE exons and optionally one or more heterologous GBE. The transformed plants are useful for producing starch with modified and improved properties, which is an important raw material and used in the food, paper and chemical industries. The present sequence encodes CC Potato SBE II, used to make transgenic plants of the invention	
XX		
CC	Sequence 2563 BP; 749 A; 462 C; 614 G; 738 T; 0 U; 0 Other;	
XX		
CC	Alignment Scores:	
XX		
CC	Pred. No.: 4.34e-293 Length: 2563	
XX		
CC	Score: 3197.00 Matches: 586	
XX		
CC	Percent Similarity: 82.78% Conservative: 82	
XX		
CC	Best local Similarity: 72.61% Mismatches: 91	
XX		
CC	Query Match: 76.69% Indels: 48	
XX		
CC	DB: 5 Gaps: 6	
XX		
CC	US-09-508-377-12 (1-768) x ABK50301 (1-2563)	
XX		
CC	2 AlathrPhealValSerGlyAlaThrLeu-----GlyValAlaArgProProAlaAla 19	
XX		
CC	Db 114 TCTACAGTGGAGCATGGGGAAGCTCTTGCTGCTGGAACCCAGAGGATAGTCTCTCA 173	
XX		
CC	20 AlaGlnProGluGluLeuGlnIleProGlu----- 29	
XX		
CC	Db 174 TCCCAACACGACCAATTGAGTTCATGAGACATCTCCAGAAATTCGCCAGCATCACT 233	
XX		
CC	30 AspIleGluGluGlnThrAlaGlu----- 37	
XX		
CC	Db 234 GATGTAGATGATTCAACATGAAACGCTAGCCAGATTAAACTGAGAACGATGACGTT 293	
XX		
CC	38 -----ValAsnMetThrGlyGlyThrAlaGlu----- 46	

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QY 402 ArgTIPrLeuGluGluTyrIysPheAspGlyPheArgPheAspGlyValThrSerMet 421
Db 1410 AGATGGTGGTGGATGATGATTCATTAATTTGATGATTTGATGGTGACATCATG 1469
QY 422 MetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAspTyrGlyGluTyrPheGly 441
Db 1470 ATGTGTACTCACCAACGATTTATCGGATTCACCTGGGAACTACGAGAAATACCTTTGGA 1529
QY 442 PheAlaThrAspValAspAlaValAlaTyrLeuMetLeuValAsnAspLeuLeuHisGly 461
Db 1530 CTCGCACTGATGTGATGCTGTGTCTATCTGATGCTGTCACAGATCTTATTCATGGG 1589
QY 462 LeuHisProAspAlaValSerIleGlyIleAspValSerGlyMetProThrPheCysIle 481
Db 1590 CTTTCCCAAGATGCAATTAACATGATGGAAGATGTTAGCGGAATGCCGACATTTGTATT 1649
QY 482 ProValProAspGlyGlyValAlaGlyPheAspTyrArgLeuHisMetAlaValAlaAspLys 501
Db 1650 CCGGTTCAAGATGGGGGTGTGGCTTGACTATCGCTGCTGATGCAATGCGATTGCTGATAA 1709
QY 502 TrpIleGluLeuLeuLysGlnSerAspGlySerTrpLysMetGlyAspIleValHisThr 521
Db 1710 TGGATTGAGTTGCTCAGAAACGGAGATGAGGATGGAGAGTGAATGATTTGTCATACA 1769
QY 522 LeuThrAsnArgArgTyrIleuGluLysCysValThrTyrAlaGluSerHisAspGlnAla 541
Db 1770 CTGACAAATGAGAGATGTCGGAAGATGTGTTTCATACGCTGAAGTCATGATCAAGCT 1829
QY 542 LeuValGlyAspLysThrIleAlaPheThrLeuMetAspLysAspMetTyrAspPheMet 561
Db 1830 CTAGTCGGATAAACTATGATGCAATCTGGCTGATGACAAAGATATGATGATTTTATG 1889
QY 562 AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMetIle 581
Db 1890 GCTCTGATGACCGCTCAACATCACTTAATGATCGTGGATGACATTCACAGATGATTT 1949
QY 582 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 601
Db 1950 AGGCTTGTAACTATGAGATTGAGAGAGAAAGGTAACCTAAATTCATGGAATGAATTC 2009
QY 602 GlyHisProGluTyrPheAspPheProArgGlyProGlnThrLeuProThrGlyLysVal 621
Db 2010 GGGCACCCCGAGTGGATTTCCCTAGGGCTGACAAACACCTCTTGATGGCTCAGTA 2069
QY 622 LeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 641
Db 2070 ATTCCCGGAACCAATTGATGATTAATGATTAATGACAGGAGATTTGACCTGGAGATGCA 2129
QY 642 AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
Db 2130 GATTATTTAAGATACCGTGGGTGCAAGATTTGACCGGGCTATGCAAGTATCTTGAAAGAT 2189
QY 662 LysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGluGluAspLys 681
Db 2190 AAAATATGAGTTTATGACTTCAGAACACCGTTCATATTCAGAAAGGATGAGAGGATAGG 2249
QY 682 ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTrpSerAsnSer 701
Db 2250 ATGATTGATTTGAAAGAAAGAACTAGTTTGTCTTAAATTTTCACTGGACAAAGAGC 2309
QY 702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrIleValAlaLeuAspSer 721
Db 2310 TATTCAGACTATCGCATAGGCTGCTGAGAGCCCTGGAATAATACAAAGGTTGCTTGACTCG 2369
QY 722 AsnAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741
Db 2370 GATGATCCACTTTGGTGGCTTTGGAGAAATGATCATATGCGGATATCTTCACTTT 2429
QY 742 GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761
Db 2430 GAAGGATGTGATGATGCTGCTGCTTCAATATATGATGACCTAGTAGAGACAGCA 2489
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Db 2490 GTGGTCTATGCACTAGTAGAGAC 2510
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Search completed: April 17, 2004, 20:10:55
Job time : 622 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 18:30:19 / Search time 5304 Seconds
(without alignments)

6275.914 Million cell updates/sec

Title: US-09-508-377-12

Sequence: 1 MATPAVSGATLGVARPPAAA.....PRFSVTPSPRTAVVYALTE 768

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Database :

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41: em_htgo_other:*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4169	100.0	2726	8 AF338432	AF338432 Trilicium
2	4119.5	98.8	2970	8 AF286319	AF286319 Trilicium
3	4113.5	98.7	2970	8 TASBA2	Y11282 T. aestivum
4	4080.5	97.9	2549	8 BT008928	BT008928 Trilicium
5	4031.5	96.7	2853	6 AR340173	AR340173 Sequence
6	4031.5	96.7	2853	6 TAU66376	TAU66376 Trilicium ae
7	3938	94.5	2554	8 AF064560	AF064560 Hordeum ae
8	3685	88.4	3015	6 E14723	E14723 Rice mRNA f
9	3685	88.4	3015	8 AB023498	AB023498 Oryza sat
10	3667	88.0	2364	6 E14724	E14724 Rice mRNA f
11	3588.5	86.1	2446	6 AR427891	AR427891 Sequence
12	3588.5	86.1	2795	8 ZMU65948	ZMU65948 Zea mays at
13	3362	80.6	2918	8 R1CBCE3	R1CBCE3 Oryza sativ
14	3362	80.6	2919	6 AR304540	AR304540 Sorghum b
15	3351.5	80.4	2664	6 AR427892	AR427892 Hordeum v
16	3351	80.3	2780	8 AF064561	AF064561 Hordeum v
17	3348.5	80.3	3549	8 PSBBRGEN	PSBBRGEN Hordeum v
18	3346	80.3	2640	6 BD071188	BD071188 Plant 11k
19	3342	80.2	2725	6 AR106495	AR106495 Sequence
20	3342	80.2	2725	6 WZEGJUCTRN	WZEGJUCTRN Corn starch
21	3342	80.1	2665	6 AR368850	AR368850 Sequence
22	3341	80.1	2665	6 AR654742	AR654742 Sequence
23	3337.5	79.3	3360	8 AB029548	AB029548 Phaseolus
24	3307.5	79.0	3090	6 A92164	A92164 Sequence 30
25	3292	79.0	2418	6 AX506177	AX506177 Sequence
26	3258	78.1	2418	6 AX651816	AX651816 Sequence
27	3258	78.1	2542	8 ATU22428	ATU22428 Arabidopsis
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29	3257.5	77.8	2913	6 A92162	A92162 Sequence 28
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31	3219	76.9	2493	8 STSBER1	STSBER1 Solanum t
32	3207	76.9	2563	6 AX256072	AX256072 Sequence
33	3197	76.7	2529	6 AS8167	AS8167 Sequence 17
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36	3192	76.6	2578	6 AS8169	AS8169 Sequence 19
37	3189	76.5	3074	6 AR123355	AR123355 Sequence
38	3189	76.5	3074	6 AR241392	AR241392 Sequence
39	3189	76.5	2982	6 AU011888	AU011888 Solanum t
40	3180	76.3	2307	6 AX755372	AX755372 Sequence
41	3164.5	75.9	2576	6 AS8166	AS8166 Sequence 16
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RESULT 1

ALIGNMENTS

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DEFINITION Triticum aestivum starch branching enzyme I1a variant mRNA,
complete cds.
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VERSION AF338432.1 GI:13447951
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PubMed
REFERENCE
AUTHORS
TITLE
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FEATURES
Source
CDS
ORIGIN
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Pred. No.: 3,72e-315 Length: 2726
Score: 4169.00 Matches: 768
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US-09-508-377-12 (1-768) x AF338432 (1-2726)
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QY 21 GlnProglugluLeuGlnIleProgluAapIleGluGluGlnThrlAglValAasMet 40
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KFSVQAPGEIPEFGIYYDPPEEKVYFQHPQPKPESLRILIESHIGMSPEKINSYA
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VTRFLSNARWMLBEYKDFRPPDGVTSMTTTHGLQMTFPGNVSEYEGPATDAVY
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SDSEWKVDIVLHILTNRWLEKCYTAAASHOALVGDYTLIAWLDKMDYPMALDRP
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NNNSYDKCRGRFDGDADFLRYHGWQEFDDQMOLHEKXGFWTSEHQYVSRGHEDKY
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ACCESSION	AF286319				
VERSION	AF286319.1	GI:11037533			
KEYWORDS					
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				
REFERENCE	McClue, K.F., Hurkman, W.J., Tanaka, C.K. and Anderson, O.D.				
AUTHORS	1 (bases 1 to 2970)				
TITLE	Starch Branching Enzymes Sbe1 and Sbe2 from Wheat (Triticum aestivum cv. Cheyenne): Molecular Characterization, Developmental Expression, and Homolog Assignment by Differential PCR				
REFERENCE	Plant Mol. Biol. Rep. 20 (2), 191-192 (2002)				
AUTHORS	2 (bases 1 to 2970)				
TITLE	Submitted (11-JUN-2000) United States Department of Agriculture, Agricultural Research Service, 800 Buchanan Street, Albany, CA 94710-1105, USA				
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ORIGIN					
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Score:	4119.50	Matches:	766		
Percent Similarity:	93.07%	Conservative:	0		
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Triticum aestivum (bread wheat)	Triticum aestivum (bread wheat)	Triticum aestivum (bread wheat)	Triticum aestivum (bread wheat)
Triticum aestivum	Triticum aestivum	Triticum aestivum	Triticum aestivum
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Nair, R.B., Baga, M., Scoles, G.J., Kartha, K.K. and Chibbar, R.N.	Nair, R.B., Baga, M., Scoles, G.J., Kartha, K.K. and Chibbar, R.N.	Nair, R.B., Baga, M., Scoles, G.J., Kartha, K.K. and Chibbar, R.N.	Nair, R.B., Baga, M., Scoles, G.J., Kartha, K.K. and Chibbar, R.N.
Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat	Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat	Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat	Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat
Plant Sci.	Plant Sci.	Plant Sci.	Plant Sci.
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Chibbar, R.N.	Chibbar, R.N.	Chibbar, R.N.	Chibbar, R.N.
Direct Submission	Direct Submission	Direct Submission	Direct Submission
Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, CANADA	Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, CANADA	Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, CANADA	Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, CANADA

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Score:	413.50
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Best Local Similarity:	92.95%
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	Gaps: 1

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LOCUS Triticum aestivum clone wdel.f.pX002.98.f1e, full insert mRNA
sequence.
ACCESSION BT008928
VERSION BT008928.1 GI:32128479
KEYWORDS FLI CDNA.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 2549)
REFERENCES
Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
Carlier,N.R., Haneley,M.K. and Hailey,C.F.
Direct Submission
Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA

FEATURES
Location/Qualifiers

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RESULT 7
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LOCUS Hordeum vulgare cultivar Bomi starch branching enzyme Iia (SbeIIa)
DEFINITION mRNA, nuclear gene encoding plastid protein, complete cds.
ACCESSION AF064560
VERSION AF064560.1 GI:3822019
KEYWORDS
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
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Poideae; Triticeae; Hordeum.
1 (bases 1 to 2554)
Sun, C., Sathish, P., Ahlandsberg, S. and Jansson, C.
The two genes encoding starch-branching enzymes Iia and Iib are
differentially expressed in barley
Plant Physiol. 118 (1), 37-49 (1998)

JOURNAL
MEDLINE
PUBMED
9733524
2 (bases 1 to 2554)
Sun, C., Sathish, P., Ahlandsberg, S. and Jansson, C.
Direct Submission
Submitted (11-MAY-1998) Stockholm University, Biochemistry,
Stockholm S-10691, Sweden
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7.. 2221
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FEATURES
source

gene
CDS

Alignment Scores:
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Best local Similarity: 98.23% Mismatches: 7
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US-09-508-377-12 (1-768) x AF064560 (1-2554)

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Qy 314 AsnPhePheAlaProSerSerArgPheGlyTyrThrProGluAspLeuLysSerLeuIleAsp 333
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 ACCESSION E14723
 VERSION E14723.1 GI:5709406
 KEYWORDS JP 1998004970-A/1.
 SOURCE
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 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriatridaceae; Oryzaceae; Oryza.
 REFERENCE
 1 (bases 1 to 3015)
 AUTHORS Baba, T., Kawasaki, T. and Ichikawa, N.
 TITLE NEW RICE GENE FOR STARCH-BRANCHING ENZYME
 JOURNAL Patent: JP 1998004970-A 1 13-JAN-1998
 MITSUI SHOKUBUTSU BIO KENKUSHO:KK, MITSUI PETROCHEM IND LTD
 COMMENT
 OS Oryza sativa (rice)
 PN JP 1998004970-A/1
 PD 13-JAN-1998
 PF 24-JUN-1998 JP 1996162983
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 C12N15/09, A01H5/00, C07H21/04, C12N9/10, C12N15/09, PC
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 ORGANISM Oryza sativa
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (sites)
 Mizuno, K., Tachibana, M., Kobayashi, E., Kawasaki, T., Funane, K.,
 Kobayashi, M. and Baba, T.
 Molecular cloning and expression analysis of a novel member of
 starch branching enzyme isoform in developing rice seeds
 Unpublished
 2 (bases 1 to 3015)
 Mizuno, K. and Baba, T.
 Direct Submission
 Submitted (09-FEB-1999) Kouichi Mizuno, University of Tsukuba,
 Institute of Agricultural and Forest Engineering, 1-1-1 Tennoudai,
 Tsukuba, Ibaraki 305-8572, Japan
 (E-mail: koum@tsakura.cc.tsukuba.ac.jp, Tel: 81-298-53-4656,
 Fax: 81-298-55-2203)
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REFERENCE			
AUTHORS	Baba,T., Kawaesaki,T. and Ichikawa,N.		
TITLE	NEW RICE GENE FOR STARCH-BRANCHING ENZYME		
JOURNAL	Patent: JP 1998004970-A 2-13-JAN-1998;		
COMMENT	MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK, MITSUI PETROCHEM IND LTD		
OS	Oryza sativa (rice)		
PN	JP 1998004970-A/2		
PD	13-JAN-1998		
PP	24-JUN-1996 JP 1996162983		
PT	BABA TADASHI, KAWASAKI TSUTOMU, ICHIRAMA NORIO PC		
C12N15/09	A01H5/00, C07H21/04, C12N5/10, C12N9/10, C12N15/09, PC		
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Location/Qualifiers

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Query Match:	87.96%	Indels:	10
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QY	91	TyrGIuLleAspProthr	110
DB	328	TACCAAAATTGCCAATG	387
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QY	151	ProGIyAlaHisSerAla	170
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QY	171	ThrMetThrArgAspArg	190
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QY	411	AspGIyPheArgPheAs	430
DB	1288	GATGGGTTTCGATTGA	1347
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DB	1468	GAAGATGTGAGGGAG	1527
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Qy      711 ArgProGlyIySerTyArgValAlaLeuAspSerAspAspAlaLeuPheGlyIyPheSer 730
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ACCESSION   AR427891
VERSION     AR427891.1 GI:40186911
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 2446)
AUTHORS     Sewalt,V.J.H. and Singletary,G.W.
TITLE       Production of modified polysaccharides
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US-09-508-377-12 (1-768) x AR427891 (1-2446)

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Qy      31 IleGluGluGlnThrIaGluValaIaAsnMetThrGlyIyThrIaGluIyLeuGluSer 50
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Qy      51 SerGluProThrGln----- 55
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Qy      56 -----GlyIleValIglyThrIleThrAsp 63
Db      257 GAGAGCCTGAGCTCTCAGAAAGTATGGAGTTGAGAGGTACTGGTGAACCAAAATTGAT 316
Qy      64 GlyValThrIyGlyValIyGluLeuValIglyIyLysProArgValIvalProIys 83
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Db      377 CCAGAGATGCGCAACAGATATATGAGATTGACCAATGTTGAAAGGCTTTCGGGCTCAC 436
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Qy      124 GlyLeuGluAlaPheSerArgGlyTyGluIyLeuGlyPheThrArgSerAlaGluGly 143
Db      497 GGTTCGATGATTTTTCAGCGCGTTACGAAAGCTTGATTACTCGCAGCGCTGAAGGT 556
Qy      144 IleThrTyArgGluTyPAlaProGlyAlaHisSerAlaAlaLeuValIglyAspPheAsn 163
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Qy      184 LeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIyIeArg 203
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Db	1697	AATGAAGAGTGCGCTTGAAGAAAGTGTGCATTAATGTCAAAATCATGATCAAGCTTGTT	1756
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QY	684	IlePheGlnIuArgGlyAspLeuValPheValPheAsnPheHisTrpSerAsnSerPhePhe	703
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
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U65948 Zea mays starch branching enzyme IIa (Sbe2a) mRNA, partial cds.			
U65948.1 GI:2340107			

SOURCE
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Eukaryote, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

REFERENCE
AUTHORS
1 (bases 1 to 2795)
Geo M., Fisher D.K., Kim K.N., Shannon J.C. and Gultinan M.J.

TITLE
Independent genetic control of maize starch-branching enzymes Ila and IId. Isolation and characterization of a Sbe2a cDNA

JOURNAL
Plant Physiol. 114 (1), 69-78 (1997)

MEDLINE
97303618

PUBMED
9159942

REFERENCE
2 (bases 1 to 2795)
Geo M., Fisher D.K., Kim K.N., Shannon J.C. and Gultinan M.J.

AUTHORS
Direct Submission

TITLE
Submitted (02-AUG-1996) Hort./Biotech.Inst., Penn State University,

JOURNAL
519 Martik, University Park, PA 16802, USA

LOCATION/Qualifiers
1..2795

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ORIGIN

Alignment Scores:

Pred. No.: 6.71e-270 Length: 2795

Score: 3588.50 Matches: 662

Percent Similarity: 88.75% Conservative: 32

Best Local Similarity: 84.65% Mismatches: 49

Query Match: 86.08% Indels: 39

DB: 8 Gaps: 4

US-09-508-377-12 (1-768) x ZM0565948 (1-2795)

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QY 31 TLeuGluGluGlnThrAlaGlnValAsnMetThrGlyGlyThrAlaGluLysLeuGluSer 50

DB 170 -----GCAGAACTG-----ACTGTGAGAGAG---ACATCC 196

51 SerGluProThrGln----- 55

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Q	224	AlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGluIleLysTyr	243
D	797	GCTCCAGGTGAATACCATCAACCGTATATATATGACCCACCTGAAAGAGAAATAT	856
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D	857	GTATTCACAAACACCTCAACCTAAGCGCCCAAGTCACTCGGATATATGATCACTGTT	916
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D	977	CCAAAGATTTAAAAAGCTTGATGATCAATGACATGACATATATGCAATCCAGAACACTCT	1036
Q	304	TyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGly	323
D	1037	TATATGCAAGCTTTGGGTACCATGTTACGAATTTTTCGCCCAAGTACCGCTTTTGGG	1096
Q	324	ThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeuValIleu	343
D	1097	ACTCCAGAGGACCTAAATCTCTTATTTGAATAAGCCATGAGCTTGCTTGATGCTT	1156
Q	344	MetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAsp	363
D	1157	ATGGAATATGTTCAATGATCATTCATCAAAATAATACCTTGATGGATGGTTTTCGAT	1216
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D	1217	GGCACCGAATACATTAATCTCATGTTGGTCCAGAGGCCATCATTTGAAATGGGATCTC	1276
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Q	424	ThrHisGlyLeuGluMetThrPheThrGlyAsnTyrGlyIleTyrPheGlyPheAla	443
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Q	444	ThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuHis	463
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Q	544	GlyAspLysThrIleAlaPheTyrLeuMetAspLysAspMetTyrAspPheMetAlaLeu	563
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Q	624	GlyAsnAsnAsnSerTyrAspLysCysArgArgPheAspLeuGlyAspAlaAspPhe	643
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RESULT 14
E08183
LOCUS E08183 2919 bp RNA linear PAT 29-SEP-1997
DEFINITION Gene of starch-branching enzyme.
ACCESSION E08183
VERSION E08183.1 GI:2176304
KEYWORDS JP 1994261767-A/1.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.
1 (bases 1 to 2919)
REFERENCE
AUTHORS Baba, T. and Shimada, H.
TITLE NEW RICE PLANT STARCH-BRANCHED ENZYMIC GENE
JOURNAL Patent: JP 1994261767-A 1 20-SEP-1994;
MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO: KK
OS Oryza sativa (rice plant)
PN JP 1994261767-A/1
PD 20-SEP-1994
PF 22-OCT-1993 JP 1993265171
PR 29-OCT-1992 JP 92P 291719
PI BABA TADASHI, SHIMADA HIROAKI
PC C12N15/54,A01H5/00,C12N5/10,C12P19/16//A23J1/10,C12N5/10; CC
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CC feature is identified by experimental;
CC feature is identified by other;
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RESULT 15

LOCUS AY304540 2664 bp mRNA linear PLN 24-JUN-2003
DEFINITION Sorghum bicolor starch branching enzyme IIB (sbeIIb) mRNA, complete cds; nuclear gene for plastid product.
ACCESSION AY304540
VERSION AY304540.1 GI:32186929
KEYWORDS
SOURCE
ORGANISM Sorghum bicolor (sorghum)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 2664)
Mutisya,J., Sabish,P., Sun,C., Andersson,L., Ahlandsberg,S., Baguma,Y., Palmqvist,S., Ochiembo,B., Amen,P. and Jansson,C. Starch branching enzymes in sorghum (Sorghum bicolor) and barley (Hordeum vulgare): Comparative analyses of enzyme structure and gene expression
J. Plant Physiol. (2003) In press
REFERENCE 2 (bases 1 to 2664)
Jansson,C. and Mutisya,J. Direct Submission
Submitted (23-MAY-2003) Plant Biology & Forestry Genetics, SU, Uppsala SE-75007, Sweden
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Pred. No.: 1,866-251 Length: 2664
Score: 3351.50 Matches: 609
Percent Similarity: 84.92% Conservative: 78
Best Local Similarity: 80.39% Mismatches: 75
Query Match: 80.39% Indels: 47
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QY 420 SerMetMetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyTyr 439
Db 1416 TCCATGATGATACCTCACCCGATTAACAAGTAACATTACGGGAGCTTCAATAGAT 1475
QY 440 PheGlyPheAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 459
Db 1476 TTGGCTTTGCCACCGATGATGATGCAAGTGGTTTACTGATCCTCGTAATATGATTAAT 1535
QY 460 HisGlyLeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPhe 479
Db 1536 CATGACATTATTCCTGAGGCTGTAAACATGGTGAAAGATGTAGTGAATGCCCTCATTT 1595
QY 480 CysIleProValProAspGlyGlyValGlyPheaspTyrArgLeuHisMetAlaValAla 499
Db 1596 GCCCTTCCTGTCAAGATGAGTGGGAGTTTGATGATCGATCGAATGCCCTGTGCT 1655
QY 500 AspIleTrpIleGluLeuLeuGlyGlnSerAspGluSerTrpLysMetGlyAspIleVal 519
Db 1656 GACAAATGATTTGATTTCTCAGCAAGTGAATGAAGCTTGGAGAATGGGTGATATTGTG 1715
QY 520 HisThrLeuThrAsnArgArgTrpLeuGluLysCysValThrTyrAlaGluSerHisAsp 539
Db 1716 CACACACTAACAAATAGAAAGTGTGGAGAGTGTGAATCTTATGCTGAAGTCAATGAT 1775
QY 540 GlnIleLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 559
Db 1776 CAAGCATTAAGTGTGACAAAGCTATTTGATTTGTTGATGACAAAGGATATGATAT 1835
QY 560 PheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLys 579
Db 1836 TTCAATGGCCCTTGATAGACCTGCACTCCTACCATTTGATCGTGGATATACATAAG 1895
QY 580 MetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGlyAsn 599
Db 1896 ATGATTAACTTATCAACAATGGTTTGAAGAGGAGGCTATCTTATTTCAATGGGAAAT 1955
QY 600 GluPheGlyHisProGluTrpIleAspPheProArgGlyProGlnThrLeuProThnGly 619
Db 1956 GAGTTTGACATCTCGAATGGAATGAAATTTTCCAAAGGTCACAAAGACTTCCAAAGTGT 2015
QY 620 LysValLeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGly 639
Db 2016 AAGTTCAATTCAGGGGATATATAACAGTTATGACAAATGCCGTGAAGATTGACCTGGGT 2075
QY 640 AspAlaAspPheLeuArgTyrHisGlyMetGlnGluPheaspGlnAlaMetGlnHisLeu 659
Db 2076 GATGGGACTATCTTAGGTATCGTGTATGCAAGAGTTGATCAGGCAATGCAACATCTT 2135
QY 660 GluGluLysTyrGlyPheMetThrSerGluHisGlnTyrValSerArgLysHisGluGlu 679
Db 2136 GAGCAAAATATGATTTCTGACATCCATCCACCAATATTTCTCGAAACATGAGAG 2195
QY 680 AspLysValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTrpSer 699
Db 2196 GATAAGATGATGTGTGTTGAAAAAGGAGATTGTGTTGTTCAACTCCACTGTAAAC 2255
QY 700 AsnSerPhePheaspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeu 719
Db 2256 AACAGCTATTGTGACTACCGATATGTGTGTGCAAAACCTGGGATGTATAAGGTGTCTTG 2315
```

Search completed: April 17, 2004, 21:39:52
Job time : 5397 secs

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Db 2316 GACTCGGACCCCTGGACTATTTGGTGGATTTGGCAGATCCATCAAGCAGAGCACTTC 2375
QY 740 ThrThrGluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArg 759
Db 2376 ACTACCGACTGTTCACATGATATAACAGCCCCCATTCCTCTGTTTATACCAAGCAGAGA 2435
QY 760 ThrAlaValValTyrAlaLeuThrGlu 768
Db 2436 ACCTGGCTGCTATGCTCCAGTGGAG 2462
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 08:35:15 ; Search time 61 Seconds
(without alignments)
3557.319 Million cell updates/sec

Title: US-09-508-377-12
Perfect score: 4169
Sequence: 1 MATFVSGATLGVANPPAAA.....PRSFVYTPSRVAVTALTE 768

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:.*
1: geneseqp1808:.*
2: geneseqp1908:.*
3: geneseqp20008:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4169	100.0	768	2	AAV06917 Starch br
2	3685	88.4	841	2	AAW41763 Rice type
3	3588.5	86.1	814	6	AAE33549 Maize BEI
4	3363	80.7	855	5	AAU76219 Wheat sta
5	3362	80.6	825	2	AAE60811 Rice star
6	3351	80.4	871	2	AAW70895 Maize bra
7	3342	80.2	799	2	AAW56489 Zea mays
8	3341	80.1	799	2	AAW19212 Corn star
9	3292	79.0	848	2	AAW62600 Starch br
10	3241.5	77.8	836	2	AAW62599 Cassava s
11	3197	76.7	842	2	AAE33804 Class A s
12	3197	76.7	842	4	AAU80169 Potato st
13	3193	76.6	878	2	AAW19113 Potato st
14	3189	76.5	847	2	AAW06400 Class A s
15	3155	75.7	858	3	AAE35092 Arabidops
16	3144	75.4	821	3	AAE35093 Arabidops
17	3135	75.2	882	2	AAW06399 Class A s
18	3080	73.9	767	7	AAE08219 Rice prot
19	3074	73.7	693	3	AAE39094 Arabidops
20	2900	69.6	592	3	AAW44410 Amino aci
21	2900	69.6	758	3	AAW84408 Amino aci
22	2879.5	69.1	888	3	AAW84416 Consensus
23	2227	53.4	481	2	AAW62650 Starch br
24	2166.5	52.0	820	2	AAE33228 Rice star

26	2156.5	51.7	906	2	AAW69300 Potato cl
27	2156.5	51.7	906	2	AAW71290 Potato st
28	2155	51.7	762	7	AAE08305 Rice prot
29	2146.5	51.5	833	3	AAE32466 Maize sta
30	2146	51.5	751	2	AAE3582 Branching
31	2146	51.5	759	2	AAW70896 Maize bra
32	2146	51.5	822	2	AAW56490 Zea mays
33	2146	51.5	822	6	AAE33548 Maize BEI
34	2146	51.5	844	2	AAW19213 Corn star
35	2140	51.3	702	4	AAE90803 Human she
36	2140	51.3	702	6	ABP71504 Amino aci
37	2134.5	51.2	807	2	AAW06916 wSBE I-D4
38	2064	49.5	834	7	AAE07804 Rice prot
39	2060	49.4	686	3	AAE49603 Glycogen
40	1965	47.1	665	4	AAE60350 Drosophila
41	1960	47.0	1101	4	AAE82299 Wheat sta
42	1870	44.9	760	4	AAU80171 Red alga
43	1642	39.4	546	6	AAE33547 Potato BE
44	1552	37.2	368	3	AAE15423 Arabidops
45	1547	37.1	367	3	AAE15424 Arabidops

ALIGNMENTS

RESULT 1
ID AAY06917 standard; protein; 768 AA.
XX
XX AAY06917;
AC
XX 17-OCT-2003 (revised)
DT
DT 05-JUL-1999 (first entry)
XX
XX
DE Starch branching enzyme II (SBE II) amino acid sequence.
XX
XX Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;
KW starch branching enzyme; starch soluble synthase; debranching enzyme;
KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
KW grain softness protein I; bacterial isoamylase; glycogen synthase;
KW wSBE I-D4 gene.
XX
XX Aegilops tauschii.
OS
XX
XX WO9914314-A1.
PN
XX
PD 25-MAR-1999.
XX
PF 11-SEP-1998; 98WO-AU000743.
XX
XX 12-SEP-1997; 97AU-00009108.
PR 20-MAR-1998; 98AU-00002509.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (AUSU) UNIV AUSTRALIAN NAT.
PA (GOOD-) GOODMAN FIELDS LTD.
XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
PI Li Z, Morell M, Rahman S;
XX WPI; 1999-229525/19.
DR
XX
XX New isolated cereal plant enzyme genes used for, e.g. expression of
PT antisense sequences of granule bound synthase.
XX
XX
PS Disclosure; Page 83-85; 171pp; English.
XX The invention relates to a novel enzyme of starch biosynthetic pathway in
CC a cereal plant, where the enzyme is selected from starch branching enzyme
CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme
CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of
CC rice or maize. The methods and products can be used for targeting

CC such as wheat or barley. They can be used for the expression of e.g.
 CC antisense sequences of granule-bound synthase (GBS), SBE II, low mol.
 CC wt. glutenin, grain softness protein 1, bacterial isomylase, bacterial
 CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be
 CC used for modifying the characteristics of starch produced by a plant. The
 CC present sequence represents the SBE II protein sequence. (Updated on 17-
 CC OCT-2003 to standardise OS field)

XX Sequence 768 AA;

Query Match 100.0%; Score 4169; DB 2; Length 768;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATFAVSATLGVARPPAAQPELQIPEDIEBQTAENVMTGTAELKESSEPTQGIYET 60
 DB 1 MATFAVSATLGVARPPAAQPELQIPEDIEBQTAENVMTGTAELKESSEPTQGIYET 60
 QY 61 ITDGVTKGVELVVGKPRVVPKPGDQKIYEIDPTLKDFRSHLDYRSEYRIRAIIDQ 120
 DB 61 ITDGVTKGVELVVGKPRVVPKPGDQKIYEIDPTLKDFRSHLDYRSEYRIRAIIDQ 120
 QY 121 HEGGLAFAFRGYEKLGTTRSAEGITTEWAPGASALVGDFFNNWNPADMTEDDYGW 180
 DB 121 HEGGLAFAFRGYEKLGTTRSAEGITTEWAPGASALVGDFFNNWNPADMTEDDYGW 180
 QY 181 EFLPNNADSPAIPIHSGRVKIRMDTSGVYDSISAMIKFSVQAPGEIPFGIYYDPPEE 240
 DB 181 EFLPNNADSPAIPIHSGRVKIRMDTSGVYDSISAMIKFSVQAPGEIPFGIYYDPPEE 240
 QY 241 EKYVFGHPQKPRESLRIYESHISMSSPEPKINSYANFRDVLPRIRKLGYNVQIMAIQ 300
 DB 241 EKYVFGHPQKPRESLRIYESHISMSSPEPKINSYANFRDVLPRIRKLGYNVQIMAIQ 300
 QY 301 EHSYVASFQHYVNFPAFSSRFCTPBDLKSIDRAHEGLLVMDIVSHSSNNTLDGLN 360
 DB 301 EHSYVASFQHYVNFPAFSSRFCTPBDLKSIDRAHEGLLVMDIVSHSSNNTLDGLN 360
 QY 361 GFGGTDTYHGGPRGHMMWDSRLFNYSWEVLRFLLSNARMWLEEKFPDFDGYTS 420
 DB 361 GFGGTDTYHGGPRGHMMWDSRLFNYSWEVLRFLLSNARMWLEEKFPDFDGYTS 420
 QY 421 MMYTHGLQMTFTGNNGYEGFATDVAVVYLMVNDLHGLHPDAVISIGEDVSGMPFC 480
 DB 421 MMYTHGLQMTFTGNNGYEGFATDVAVVYLMVNDLHGLHPDAVISIGEDVSGMPFC 480
 QY 481 IVPDGGVGDYRLHMAVADKWITLLKQSDSMKMGDI VHTLTNRMLEKCVTAESHDQ 540
 DB 481 IVPDGGVGDYRLHMAVADKWITLLKQSDSMKMGDI VHTLTNRMLEKCVTAESHDQ 540
 QY 541 ALVGDKTIAMFLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVTMGHGBGYLNFNGNE 600
 DB 541 ALVGDKTIAMFLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVTMGHGBGYLNFNGNE 600
 QY 601 FGHPEWIDPRGPQTLPTGKVLPGNNNSYDKCRRRFDIGDADFLRHYGQGEEDQMOHLE 660
 DB 601 FGHPEWIDPRGPQTLPTGKVLPGNNNSYDKCRRRFDIGDADFLRHYGQGEEDQMOHLE 660
 QY 661 EKYGFMTSEHQYVRKHEEDKVIIFERGDIVFVNFHNSNFFEDRVGCSRGKXKVALD 720
 DB 661 EKYGFMTSEHQYVRKHEEDKVIIFERGDIVFVNFHNSNFFEDRVGCSRGKXKVALD 720
 QY 721 SDDALFCGFSRLDHDVDYFTEHHPDNRPFSFVYTPERTAVVVALTE 768
 DB 721 SDDALFCGFSRLDHDVDYFTEHHPDNRPFSFVYTPERTAVVVALTE 768

DT 25-MAR-2003 (revised)
 DT 01-MAY-1998 (first entry)
 XX Rice type IV starch branching enzyme.
 DE Rice type IV starch branching enzyme; amylopectin synthesis.
 XX Rice; type IV starch branching enzyme; amylopectin synthesis.
 XX Oryza sativa.
 OS Oryza sativa.
 PN JP10004970-A.
 XX 13-JAN-1998.
 PD 24-JUN-1996; 96JP-00162983.
 PF 24-JUN-1996; 96JP-00162983.
 PR 24-JUN-1996; 96JP-00162983.
 PA (MTS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
 PA (MITK) MITSUI TOATSU CHEM INC.
 DR WPI; 1998-133625/13.
 DR N-PSDB; AAV05639.
 XX Rice starch branching enzyme gene - synthesises amylopectin to yield high
 PT quality starch.
 PS Claim 1; Page 5-8; 13pp; Japanese.
 CC The present sequence is the rice type IV starch branching enzyme, which
 CC has the ability to synthesise amylopectin. The quality of starch is
 CC improved by the use of the protein. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 CC XX
 SQ Sequence 841 AA;

Query Match 88.4%; Score 3685; DB 2; Length 841;
 Best Local Similarity 88.1%; Pred. No. 0;
 Matches 668; Conservative 37; Mismatches 43; Indels 10; Gaps 2;

QY 21 QPEELQIPED-----IEEQ-----TAEVMTGTAEKLSSEPTQGIYETITDGVTKGVK 70
 DB 83 QPEEQIPDDNKVKPFESEELPAVAFASIKVYAEKLSSEVITQIEENVTEGVIRKAD 142
 QY 71 ELVGEKPRVVPKPGDQKIYEIDPTLKDFRSHLDYRSEYRIRAIIDHGGLEAFSR 130
 DB 143 EPTVEDKPRVTPPPGQGIYIDPVLBGRFRLHDYRSEYKMRRAIDHGGLEAFSR 202
 QY 131 GYEXKGFTRSAGITTYREWAPGASALVGDFFNNWNPADMTEDDYGWEIFLPNNADG 190
 DB 203 GYEXKGFTRSAGITTYREWAPGASALVGDFFNNWNPADMTEDDYGWEIFLPNNADG 262
 QY 191 SPAIPHSGRVKIRMDTSGVYDSISAMIKFSVQAPGEIPFGIYYDPPEEKYVFGHP 250
 DB 263 SPAIPHSGRVKIRMDTSGVYDSISAMIKFSVQAPGEIPFGIYYDPPEEKYVFGHP 322
 QY 251 KRPESLRITESHIGSSPEPKINSYANFRDVLPRIRKLGYNVQIMAIQEHSSYASFGY 310
 DB 323 KRPNSLRITESHIGSSPEPKINTYANFRDVLPRIRKLGYNVQIMAIQEHSSYASFGY 382
 QY 311 HTNFPAPSRFGTPEPDLKSLIDRAHEGLLVMDIVSHSSNNTLDGLNGFQGTDRHYF 370
 DB 383 HTNFPAPSRFGTPEPDLKSLIDRAHEGLLVMDIVSHSSNNTLDGLNGFQGTDRHYF 442
 QY 371 HGGPRGHMMWDSRLFNYSWEVLRFLLSNARMWLEEKFPDFDGYTSMTYTHGLQW 430
 DB 443 HGGPRGHMMWDSRLFNYSWEVLRFLLSNARMWLEEKFPDFDGYTSMTYTHGLQW 502
 QY 431 TPTGNGEYFGPATDVAVVYLMVNDLHGLHPDAVISIGEDVSGMPTFCIPVDGGVGF 490
 DB 503 AFTGNGEYFGPATDVAVVYLMVNDLHGLHPDAVISIGEDVSGMPTFCIPVDGGVGF 562
 QY 491 DYRLHMAVADKWITLLKQSDSMKMGDI VHTLTNRMLEKCVTAESHDQALVGDXTIAF 550

RESULT 2
 AA41763
 ID AA41763 standard; protein; 841 AA.
 AC
 XX AA41763;

D	563	DYRLHMAVPDKMIELLKQSDSEYWKGDIVHTLTNRMSSEKCVTAASHQALVGDKTIAF	622
Q	551	WLMXKMDVFNALDRPSTPRIDRGIALHKMTLVMGSGEGVLNMGNEFGHPEKIDFP	610
D	623	WLMKMDVFNALDRPSTPRIDRGIALHKMTLVMGSGEGVLNMGNEFGHPEKIDFP	662
Q	611	RGPOTLPTGKALPGNNNSYDKCRRRFDLGADPLRYHGMQEPDQAMQHEEKYGFMTSEH	670
D	683	RGPSLIRPGSVLPGNMYSPDKCRRRFDLGADALRYHGMQEPDQAMQHEEKYGFMTSEH	742
Q	671	QYVSRKHEEDKYLIERGDLVFNVFNHMSNSFFDRVCGSRPKYKVALDSDALRGGFS	730
D	743	QYISKHEEDKYLIERGDLVFNVFNHMSNSFFDVAVGGLKPKQKYLIVDSDGLRGGFS	802
Q	731	RLDHDVDFTEHPPHNDNRPSFSVTPSRATVAVALTE	768
D	803	RLDHDVDFTEHPPHNDNRPSFSVTPSRATVAVALTE	840

RESULT 3
AAE33549
ID AAE33549 standard; protein; 814 AA

AC	AAE33549;
XX	
DT	16-APR-2003 (first entry)
XX	
DE	Maize BEI protein #2.

KW Transgenic; amylose; BE; R1 protein; starch; maize
 KN enzyme.

OS Zea mays

PN WO2002101059-A2.

PD 19-DEC-2002

PF 07-JUN-2002; 2002WO-EP006265.

PR 12-JUN-2001; 2001DE-01028363.

PA (FARB) BAYER CROPSCIENCE GMBH.

PI Uwer U, Froberg C, Pilling J, Landschuetze V;
.....

DR WPI; 2003-148812/14.

Novel transgenic plants and plant cells capable of synthesizing high

PT reduction of activity of branching enzymes I and II and R1 proteins.

PS Disclosure; Col 89-93; 47pp; English.

CC The invention relates to transgenic plants and plant cells capable of
CC synthesizing high amylose starch comprising a genetic modification which
CC leads to reduction of activity of branching enzymes (BE) I and II and RI
CC proteins. The invention is useful for producing starch, by extracting
CC starch from transgenic plant and/or from starch-storing parts of such a
CC plant and/or from a plant cell such as transgenic plant cell. The present
CC sequence is maize Bt1 protein

SQ Sequence 81.4 AA;

Query Match	86.1%;	Score 3588.5;	DB 6;	Length 814;
Best Local Similarity	84.7%;	Pred. NO. 0;		
Matches 662;	Conservative 35;	Mismatches 49;	Indels 39;	Gaps 4

QY LGVAREPAAAGBELQIPEDIEQTAEVNTGTGAETKESSEPT-----55
11 |||||
DB 38 LSSAEPVDIDBELQIPE----AEL-----TVEK-TSSSPITTSANVAEASSGVEAL 85

QY 56 -----GIVETITDGVTKVKELVVGKEKPRVVPKPGDGQKIYEIDPTLKDFRSH 103

Db	86	ERPELSEVIGVGCGGKTKIDGAGIKAKRPALEBKRVLPEDDGGRIITEIDMLSGFRCH	145
QY	104	LDVRYSEYRIRAIADHGGGLIAPSRGYEKLGFTRSAEGITTYRMAFQASHALVGDN	163
Db	146	LDVRYSEYKRLRAAIDHGGGLDAPFSREYEKLGFRSAEGITTYRMAAGAYPALVGDN	205
QY	164	MMNNADMPHDDAGWMEIFLNNADGSPALPHGSRVATIMDTPSGVXDSISAMIKFSVQ	223
Db	206	NNNNPADMAANEAGWMEIFLNNADGSPALPHGSRVATIMDTPSGVXDSISAMIKFSVQ	265
QY	224	APGEIPFNGIYYDDPEBEKYVFOHPQRPESLRIYESHIQMSDEPKINSYANPDEVL	283
Db	266	APGEIPYNGIYYDDPEBEKYVFKHPQRPXSLRIYESHVQMSDEPKINTYANPDEVL	325
QY	284	FRIRKLTGNAVOIMAIQSHSYASGCHYVTPFASSSPGPEDEKLILDRANHELGLVL	343
Db	326	PRIKLTGNAVOIMAIQSHSYASGCHYVTPFASSSPGPEDEKLILDKNHEGLVL	385
QY	344	MDIYHSHSNNTLDGLNFGDGTDTYFHGSPRGHMMDSRLFNYSMEVLNELLNARM	403
Db	386	MDIYHSHSNNTLDGLNFGDGTDTYFHGSPRGHMMDSRLFNYSMEVLNELLNARM	445
QY	404	WLEBYKDFGFRFDDVTSMTYTHHGLQMTFTQNYGEYFGFPAIDVDVATYMLVNDLIGHH	463
Db	446	WLEBYKDFGFRFDDVTSMTYTHHGLQMTFTQNYGEYFGFPAIDVDVATYMLVNDLIGHH	505
QY	464	PDAYSIGDVGMPFFCIYPVDGGVGPYRLHMAVADKMLELXQSDSEMKGGDIYHTLT	523
Db	506	PEAVSIGDVGMPFFCIYPVODGGVGFYRLHMAVADKMLELXQSDSEWBGDIYHTLT	565
QY	524	NRPMLEKCVTTAESHDDALVGDKTIAFMLDKMTDPMALDDBSTPRLDRGIALHXMRL	583
Db	566	NRPMLEKCVTTAESHDDALVGDKTIAFMLDKMTDPMALDDBSTPRLDRGIALHXMRL	625
QY	584	VTMGLGGEGYLANFNGNEFGHEPMLDPFPGPQTLPGFKYULPGNNNSYDKRRRRPDLGDAP	643
Db	626	VTMGLGGEGYLANFNGNEFGHEPMLDPFPGPQTLPGKSVLPGNNSYDKRRRRPDLGDAD	685
QY	644	LRHGMQFDDOMQMLBEKYGFMTESEHQVSKHEBDKYLIFERGDLVVFVFNHMSNPF	703
Db	686	LRHGMQFDDOMQMLBEKYEFMTSDHSVSKHEBDKYLIFERGDLVVFVFNHMSNSVF	745
QY	704	DYRVGCSRPGRKYVALDSDDALFGGFSRLDHDVDYFTTEHPRDNRPRSGSVTTPSTAYV	763
Db	746	DYRVGCSRPGRKYKYLVDSDDDLFGGFSRLDHDAEYFTADWPHDNRCPSPSVAPBSRTAYV	805
QY	764	YA 765	
Db	806	YA 807	

RESULT 4
AAU76219
ID AAU76219 standard; protein; 855 AA

DT 08-MAY-2002 (first entry)

DE wheat starch branching enzyme IIb protein from clone wdk2c_pk009.j17.

KW wheat; starch branching enzyme; starch synthesis
 wdk2c.pk009.j17; antibody; gene mapping; enzyme.

Triticum aestivum.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
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11	11	11
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95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

/note= "This sequence is shown in 'sequence ID no. 2 and is specifically claimed in claim 2 of the specification"

PN US2002002713-A1

XX 03-JAN-2002.
 PD 23-FEB-2001; 2001US-00792127.
 XX 01-MAR-2000; 2000US-0186098P.
 XX (ALIE/) ALIEN S M.
 PA (BECK/) BECKLES D M.
 PA (BUTL/) BUTLER K H.
 PA (PEAR/) PEARLSTEIN R W.
 PI Allen SM, Beckles DM, Butler KH, Pearlstein RW,
 DR WPI; 2002-178959/23.
 XX N-PSDB; ABX15494.
 PT Novel isolated polypeptide having starch iib enzyme activity, useful for
 PT preparing antibodies to the proteins which are used to detect the
 PT polypeptides in situ in cells or in vitro in cell extracts.

Claim 2, Fig 1, 27p; English.

This invention relates to the cDNA and protein sequences of a novel wheat starch branching enzyme iib enzyme. Starch branching enzymes are responsible for the formation of alpha 1-6 linkages in amylopectin in the starch synthesis pathway. The nucleotide sequence of the invention is useful for producing a transgenic plant expressing the starch branching enzyme. The protein sequence is useful for preparing antibodies against starch branching enzyme iib protein, which are useful for detecting the proteins in situ in cells or in vitro in cell extracts. The protein is also useful for selecting an isolated polynucleotide that affects the level of expression of a starch branching enzyme iib protein or enzyme activity in a plant cell. All or substantial portion of the nucleotide sequence can be used as probe for genetic and physical mapping of the genes and can be used as markers for traits linked to those genes. This information is useful in plant breeding in order to develop lines with desired phenotypes. A polynucleotide fragment is useful for isolating cDNAs and genes encoding homologous proteins from the same or other plant species. They are also useful as DNA hybridisation probes or as polymerase chain reaction (PCR) amplification primers. The fragments are also useful for creating transgenic plants and may be useful as restriction fragment length polymorphism markers. Nucleic acid probes derived from the cDNA sequence may also be used for physical mapping or for fluorescence in situ hybridisation (FISH) mapping. The present sequence represents the wheat starch branching enzyme iib protein encoded by the cDNA from clone wdk2c.pk009.117

XX Sequence 855 AA:

Query Match 80.7%; Score 3363; DB 5; Length 855;

Best Local Similarity 79.5%; Pred. No. 1.1e-306;

Matches 607; Conservative 75; Mismatches 68; Indels 14; Gaps 4;

QY 7 SGATLGYAPPAAGP-----EIQIPEDIEQTAQVAMTGTAKLSSSEPTQGIIVETI 61
 DB 98 SGGT-----PESIDGPFQVDSDDLKP-FIDET--SLQDGGEDSINSSEFNQVSEID 148
 QY 62 TDGVTGKVELVGEKPRVVPKPGDGQKIYEIDPTLKDQFRSHLDYRSEYRIRRAIIOH 121
 DB 149 AEDTSRMDKESSTREKRIILPPENGQOIYEIDPLRPFKYLERYSLYRIRSIDBH 208
 QY 122 EGGLEAFSGRGYKLGFTFSAGETTYREWAPGASALATVDPPNNPNADTFTRDYGVWE 181
 DB 209 EGGMDVFSRGYKLGFTFSAGETTYREWAPGASALATVDPPNNPNADTFTRDYGVWE 268
 QY 182 IFLNNNDGSPALIPGSRVKIRMDTPSGVKDSISAMIKSVQAPGIPNGIYYDPPEE 241
 DB 269 IFLNNNDGSPALIPGSRVKIRMDTPSGVKDSISAMIKSVQAPGIPNGIYYDPPEE 328
 QY 242 KYVFQHPQPKPESIRIYESHIGMSPEEKINSYANFRDEVLPRIKELGYNAVOIADCE 301
 DB 329 KYVFQHPQPKPESIRIYESHIGMSPEEKINSYANFRDEVLPRIKELGYNAVOIADCE 388

QY 302 HSYVAFGYHTVTFPAPSSRFGTPEDLKSILIDRAHELGLVLMDIVSHSSNNITLDGLNG 361
 DB 389 HSYVAFGYHTVTFPAPSSRFGTPEDLKSILIDRAHELGLVLMDIVSHSSNNITLDGLNG 448
 QY 362 FDGTDTHYFHGSGPRGHMMWDSRLFNYSWEYARELISNAPWLEBYKXDFGFDVTSW 421
 DB 449 FDGTDTHYFHGSGPRGHMMWDSRLFNYSWEYARELISNAPWLEBYKXDFGFDVTSW 508
 QY 422 MYTHGLQMTTTCNGEYFPGATVDVAVYMLVNDLHGLHPDAYSIGEDVSGMPTFC 481
 DB 509 MYTHGLQMTTTCNGEYFPGATVDVAVYMLVNDLHGLHPDAYSIGEDVSGMPTFC 568
 QY 482 FVPDGGVGFEDYRLHMAVADKMTIELLKQSDSWKMGDIYHTLTNRRLKCVYAESHDQ 541
 DB 569 FVPDGGVGFEDYRLHMAVADKMTIELLKQSDSWKMGDIYHTLTNRRLKCVYAESHDQ 628
 QY 542 LVGDKTIAFWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGSEGYLNFNGNEF 601
 DB 629 LVGDKTIAFWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGSEGYLNFNGNEF 688
 QY 602 GHPWIDPPRGQOTLPTGKVLPGNNNSYDKCRRRDLGADLRLRYHGMQEFQAMQHLE 661
 DB 689 GHPWIDPPRGQOTLPTGKVLPGNNNSYDKCRRRDLGADLRLRYHGMQEFQAMQHLE 748
 QY 662 KYGFWTSRHOYVSRKHEBDKVIIFERGLVFEYFNHMSNSFFDYRGSGRPGKYKVALDS 721
 DB 749 KYGFWTSRHOYVSRKHEBDKVIIFERGLVFEYFNHMSNSFFDYRGSGRPGKYKVALDS 808
 QY 722 DDALFGFSRLDHDVDYFTTEHFDNRPSPSVYTPSRITAVYVA 765
 DB 809 DAGLFGGRIRHHTAHTSDCQHNRPSPSVYTPSRITAVYVA 852

RESULT 5

AA060811 ID AA060811 standard; protein; 825 AA.

AA060811; 05-JUL-1995 (first entry)

Rice starch branching enzyme.

Starch branching enzyme; rice; starch content.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Key Location/Qualifiers
 Peptide 1..65
 Protein /label=transit_peptide
 65..825
 /label=starch_branching_enzyme
 JP06261767-A.
 20-SEP-1994.
 22-OCT-1993; 93JP-00265171.
 29-OCT-1992; 92JP-00291719.
 (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
 WPI; 1994-337418/42.
 N-PSDB; AA073750.
 New gene of branching enzyme of rice starch - useful for increasing starch yield of grain.
 Claim 1, Page 9-12; 13p; Japanese.
 The rice starch branching enzyme (AA060811) and cDNA encoding it have

QY 413 FRPDGVTSMYTHHGLQMTFTNGYGEFGFATVDVAVYLMVNDLHGHPDAVISED 472
 Db 444 FRPDGVTSMYTHHGLQMTFTNGYGEFGFATVDVAVYLMVNDLHGHPDAVISED 503
 QY 473 VSGMPTFCIPVPPGCVGPDYRLHMAVADKWTLELKQSDGSMKMDIVHTLNNRRLKCV 532
 Db 504 VSGMPTFCIPVPPGCVGPDYRLHMAVADKWTLELKQSDGSMKMDIVHTLNNRRLKCV 563
 QY 533 TYAESHDQALVGDXTIAFWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGSEG 592
 Db 564 TYAESHDQALVGDXTIAFWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGSEG 623
 QY 593 YLNFMGNEFGHPMTIDPRGPQTLPTGKVLPGNNNSYDKCRRRPDLGADYLRHGMQEF 652
 Db 624 YLNFMGNEFGHPMTIDPRGPQTLPTGKVLPGNNNSYDKCRRRPDLGADYLRHGMQEF 683
 QY 653 DOAMOHLEEKYGFMTSEHGYVSRKHEEDKVIIFERGLVFEVNFHMSNSFFDYRGVCSRP 712
 Db 684 DOAMOHLEEKYGFMTSEHGYVSRKHEEDKVIIFERGLVFEVNFHMSNSFFDYRGVCSRP 743
 QY 713 GKYKVALDSDDALFGGFSRLDHDVYFTTEHPHDNRPRSFSVYTPSRVAVYALTE 768
 Db 744 GKYKVALDSDDALFGGFSRLDHDVYFTTEHPHDNRPRSFSVYTPSRVAVYALTE 799

RESULT 7

AAW56489 ID AAW56489 standard; protein; 799 AA.

AAW56489; 11-SEP-1998 (first entry)

11-SEP-1998 (first entry)

Zea mays starch branching enzyme II.

SEB; starch-encapsulating region; fusion vector.

starch branching enzyme II; glucosyl transferase.

Zea mays.

WO9814601-A1.

09-APR-1998.

30-SEP-1997; 97WO-US017555.

30-SEP-1996; 96US-0026855P.

(EXSE-) EXSEED GENETICS LLC.

Keeling P, Guan H;

WPI; 1998-240100/21.

N-PSDB; AAV29757.

Hybrid polypeptide comprising starch-encapsulating region and protein -

useful for, e.g. producing protein(s) resistant to degradation by stomach

acids.

Example 2; Page 43; 156pp; English.

The sequence is that of starch branching enzyme II. It can be used in the

production of a hybrid polypeptide comprising a starch-encapsulating

region (SEB) fused to a payload protein. The hybrid polypeptide can be

used to make modified starches comprising the payload protein, selected

from, e.g. hormones, growth factors, antibodies, enzymes, dyes,

immunoglobulins, etc. The modified starch can also be used to provide

grain feeds enriched in amino acids. By encapsulating the payload protein

in starch, it is more resistant to degradation by stomach acids

Sequence 799 AA;

Query Match 80.2%; Score 3342; DB 2; Length 799; XX

Best Local Similarity 78.4%; Pred. No. 9e-305; Matches 608; Conservative 67; Mismatches 79; Indels 22; Gaps 4;

QY 4 FAVSGATLGV-----ARPPAAQPEELQIPEDIEQTAEVMTGTAEKLESSE----- 52
 Db 35 FLTRGARVCGSGTHGAMRAAAAARAKAVWVEGEND-----GLASRADSAQFQDEL 85
 QY 53 PFGIVETITDGVTKGKVLVNGEKRVYKPKPDGQKIYEDITLDFRRLDVRYSYR 112
 Db 86 EVDISEETTCGA--GVAQAQALNRYVPPPSDQKIFQIDPMLQGYKTHLEYRILYR 143
 QY 113 RIRPAIDQHEGGLAEAFSRGEKLGFTPSAEGITYREMAPGASAAVYGDPRNNPNADTM 172
 Db 144 RIRSDIDHEGGLAEAFSRGEKGFNASADGITYREMAPGAFSAALVGVVNMMDPNADM 203
 QY 173 TRDDYGVWEIPLPNNADGSPALPHGSRVKIRMDTPSGVQDSISAMIFSVQAPPEIPNG 232
 Db 204 SKNEFGWEIPLPNNADGSPALPHGSRVKIRMDTPSGVQDSISAMIFSVQAPPEIPNG 263
 QY 233 IYDPEEEKYVQHPQPKRPSRLTYESHIGSSPEPKINSYANFRDEVLPRIKRLGYN 292
 Db 264 IYDPEEEKYVQHPQPKRPSRLTYESHIGSSPEPKINSYANFRDEVLPRIKRLGYN 323
 QY 293 AVQIMAIQESHYSYASFGYHVTNFFAPSSRFTEDELKSLIDRAHELGLVLMDIVSHSS 352
 Db 324 AVQIMAIQESHYSYASFGYHVTNFFAPSSRFTEDELKSLIDRAHELGLVLMDIVSHSS 383
 QY 353 NNTLDGLNGFDGDTIYFHGSGRHHMMDSRLFNIGSWBYLRPLLSNARWMLSEYKDG 412
 Db 384 NNTLDGLNGFDGDTIYFHGSGRHHMMDSRLFNIGSWBYLRPLLSNARWMLSEYKDG 443
 QY 413 FRPDGVTSMYTHHGLQMTFTNGYGEFGFATVDVAVYLMVNDLHGHPDAVISED 472
 Db 444 FRPDGVTSMYTHHGLQMTFTNGYGEFGFATVDVAVYLMVNDLHGHPDAVISED 503
 QY 473 VSGMPTFCIPVPPGCVGPDYRLHMAVADKWTLELKQSDGSMKMDIVHTLNNRRLKCV 532
 Db 504 VSGMPTFCIPVPPGCVGPDYRLHMAVADKWTLELKQSDGSMKMDIVHTLNNRRLKCV 563
 QY 533 TYAESHDQALVGDXTIAFWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGSEG 592
 Db 564 TYAESHDQALVGDXTIAFWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGSEG 623
 QY 593 YLNFMGNEFGHPMTIDPRGPQTLPTGKVLPGNNNSYDKCRRRPDLGADYLRHGMQEF 652
 Db 624 YLNFMGNEFGHPMTIDPRGPQTLPTGKVLPGNNNSYDKCRRRPDLGADYLRHGMQEF 683
 QY 653 DOAMOHLEEKYGFMTSEHGYVSRKHEEDKVIIFERGLVFEVNFHMSNSFFDYRGVCSRP 712
 Db 684 DOAMOHLEEKYGFMTSEHGYVSRKHEEDKVIIFERGLVFEVNFHMSNSFFDYRGVCSRP 743
 QY 713 GKYKVALDSDDALFGGFSRLDHDVYFTTEHPHDNRPRSFSVYTPSRVAVYALTE 768
 Db 744 GKYKVALDSDDALFGGFSRLDHDVYFTTEHPHDNRPRSFSVYTPSRVAVYALTE 799

RESULT 8

AAW19212 ID AAW19212 standard; protein; 799 AA.

AAW19212; 10-SEP-1997 (first entry)

10-SEP-1997 (first entry)

Corn starch branching enzyme IIb.

Starch branching enzyme IIb; SEBIIb; corn; maize; antisense; amylopectin;

transgenic plant; pBE240.

Zea mays.

WO9722703-A2.

Query Match 80.2%; Score 3342; DB 2; Length 799; XX

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us-09-508-377-12.rag

Page 7

26-JUN-1997.
12-DEC-1996; 96WO-US019678.
20-DEC-1995; 95US-0009113P.
(DUPO) DU PONT DE NEMOURS & CO E I.
Hubbard NL, Klein TM, Broglie KE;
WPI, 1997-341694/31.
N-PSDB; AAT69729.
Transgenic corn in which grain derived starch fine structure is
controlled - specifically branch chain distribution of amylopectin,
useful in preparation of thickened foodstuff.
Example 1; Page 50-53; 92pp; English.
Corn starch branching enzyme IIb (SBEIIb) (AAW19212) is an isoform of
starch branching enzyme that shows higher rates of branching with
amylopectin rather than amylose as substrate. A cDNA insert (AAT69729) in
plasmid clone pBR240 that expresses SBEIIb has been used as a starting
point in the assembly of DNA constructs (see also AAT69730, AAT69736-37)
designed to achieve suppression of SBEIIb expression in transgenic corn
plants, and thereby to produce novel starches that have properties
beneficial in food and industrial applications

Sequence 799 AA;
Query Match 80.1%; Score 3341; DB 2; Length 799;
Best Local Similarity 78.4%; Pred. No. 1.1e-304;
Matches 608; Conservative 67; Mismatches 79; Indels 22; Gaps 4;

4 FAVSGATLGV-----ARPPAAQPEELQIPEDIEEQTAENVMTGTAKESSE----- 52
35 FLTRGARVCGSGTHGARRAARAAAKAVMVEGEND-----GLASRADSAQFOSDEL 85
53 PROGIYETITDGTGKVELVGEKPRVVPKPGDGQKIYEIDPTLKDFRSHLDYRSEYR 112
86 EWPDISETTCGA--GVADAQALNRVVPPEPSDQKI FQIDPVLGKTHLEIRYSIKR 143
113 RIRPAIDQHEGEGLEAFSGRYEKLQFTRSABGITYREMAFGAHSALVGDENNPNADTM 172
144 RIRSDIDHEHGGELEAFSGRYEKLQFTRSABGITYREMAFGAHSALVGDENNPNADRM 203
173 TRDDYGVMEIFLPPNADGSPAIPIHSGSVKIRMDTPSGVKDISAMIKRSVQAPGEIPNG 232
204 SKKEFGWEIFLPPNADGSPAIPIHSGSVKIRMDTPSGVKDISAMIKRSVQAPGEIPYDG 263
233 IYDPEEKEKRVQHPKPKPESTRIYESHIGMSPEPKIXSYNFRREVPRIRLGYN 292
264 IYDPEEKEKRVQHPKPKPESTRIYESHIGMSPEPKIXSYNFRREVPRIRLGYN 323
293 AVOIMAIQESHYVAFGVHVTNFPAPSGRFGTPEDLKSLIDRAHELGLVIMDIVSHSS 352
324 AVOIMAIQESHYVAFGVHVTNFPAPSGRFGTPEDLKSLIDRAHELGLVIMDIVSHSS 383
353 NNTLDGNGFDGDTTHYFHGGPRGHMMWDSRLFNYSWMEVLRFLSNARWLEEKYKPDG 412
384 NNTLDGNGFDGDTTHYFHGGPRGHMMWDSRLFNYSWMEVLRFLSNARWLEEKYKPDG 443
413 FRPBGVSNMYTHHGLQMTFTGNGGEYGFAPTDVAVVYLMVNDLHGLHPDAVSIGD 472
444 FRPBGVSNMYTHHGLQMTFTGNGGEYGFAPTDVAVVYLMVNDLHGLHPDAVSIGD 503
473 VSGMPFCIPVDPGCVGDFYRLHNAVADKWI ELLKQSDSWKMGDI VHTLNRNLEKCV 532
504 VSGMPFCIPVDPGCVGDFYRLHNAVADKWI ELLKQSDSWKMGDI VHTLNRNLEKCV 563
533 TYAESHQALVGDKTIAFWLMDKMYDPMALDRPSTPIIDGIALHKIKRLVTMGLGEG 592

593 YLNMENEPFGHPWIDPPRGPQLPTGKVLPGNNNSYKCRRRPDLGADAFIRHGMQEF 652
624 YLNMENEPFGHPWIDPPRGPQLPTGKVLPGNNNSYKCRRRPDLGADAFIRHGMQEF 683
653 DQAMQHLEKXGEMTSEHQYVSRKHEKXVIFERGDVFNENFMNSFFDYRVGCSRP 712
684 DQAMQHLEKXGEMTSEHQYVSRKHEKXVIFERGDVFNENFMNSFFDYRVGCSRP 743
713 GKXKALDSDDALFGFSRLDHDVDYFTTEHPHNRPRPSFYTPSRRTAVVYALTE 768
744 GYKXVLDSDAGLFGFSRIRHAAHEFTALDCSHDRPFYSSSYTTSRTCVVYAPVE 799

RESULT 9
AAW62600
ID AAW62600 standard; protein; 848 AA.
AC AAW62600;
DT 21-SEP-1998 (first entry)
XX Starch branching enzyme II (SBE II).
XX Starch branching enzyme; SBE; cassava.
XX Manihot esculenta.
FH Key Location/Qualifiers
FT Misc-difference 143..145
FT note="proline elbow"
XX W09820145-A2.
PD 14-MAY-1998.
XX 04-NOV-1997; 97WO-GB003032.
XX 05-NOV-1996; 96GB-00023095.
XX (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
PI Jobling SA, Safford R;
XX WPI, 1998-286958/25.
DR N-PSDB; AAW62600.
XX Starch branching gene from cassava - useful for producing altered plants
giving modified starch.
PS Claim 1; Fig 13; 67pp; English.

Query Match 79.0%; Score 3292; DB 2; Length 848;
Best Local Similarity 77.3%; Pred. No. 5.1e-300;
Matches 595; Conservative 71; Mismatches 72; Indels 32; Gaps 4;
23 BELQIPEP-----IEQTAENVMTG-----GIAEKL-----ESSSEPTQGI 58
68 EKVLPVDDQIDGSSSTYQLETTGVLESQVLGDASLVMEDDKVVEDEYKESVPLH 127
59 ETTDGVTKGVKELVVGKPRVVPKPGDGQKIYEIDPTLKDFRSHLDYRSEYRIRPAI 118
128 ETTISIKSE-----SKRSTIPPGSGQRITIDIDPSLNGFRGLDLYRSQYKRLREI 179

ID	AAR93804
AC	AAR93804 standard; protein; 842 AA.
DJ	AAR93804;
DT	03-MAY-1997 (first entry)
KW	Class A starch branching enzyme (direct sequencing).
XX	
KM	Starch branching enzyme; SBE; class A; class B; Solanum tuberosum; amylose; viscosity; potato.
OS	Solanum tuberosum.
FH	Key Location/Qualifiers
FT	Misc-difference 43 //label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 304 //label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 348 //label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 594 //label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 610 //label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 747 //label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 811 //label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 830 //label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 832 //label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 838 //label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 839 //label= OTHER
FT	/note= "encoded by ambiguous codon"
PN	WO9634968-A2.
PD	07-NOV-1996.
PF	03-MAY-1996; 96WO-GB001075.
PR	05-MAY-1995; 95GB-00009229. 10-APR-1996; 96GB-00007409.
PA	(NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
PI	Cooke D., Debet M., Gidley MJ., Jobling SA, Safford R, Sidebottom CM, Westcott RJ,
DR	WPI; 1996-506170/50. N-PDSB; AAT17267.
PT	New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of starch; for use in food, biodegradable products, adhesives, etc.
SS	Example 1; Fig 9, 142pp; English.

CC class ABE mols., a flexible N-terminal domain, is found, which is not
CC found in class B mols. The nucleotide sequence encoding this protein was
CC obtained by direct sequencing of PCR fragments amplified from first
CC strand cDNA. Nucleotides which could not be unambiguously assigned are
CC indicated using standard IUPAC notation. Where this uncertainty affects
CC the predicted amino acid sequence x is used in the sequence

Sequence 842 AA:

Query Match	Score	DB 2	Length
76.7%	3197	842	

Best Local Similarity 72.6%; Pred. NO. 4.4e-291;
Matches 586; Conservative 80; Mismatches 93; Indels 48; Gaps 6;

2 ATFAVSGATL--GVARPPAAQPEELQIPE-----DIEEQTAE----- 37

Db 30 STVAASGKLVPGXQSDSSSSSTDQFEFTEFSPENSPASTVDVDSSTMEHASQIKTENDDV 89

QY 38 ---VNMTGTAE-----KLESSEPTGIVETITDGVTKGVKELVGEKPRV 81

Db 90 EPSSDLTGSVEELDFASSLQLEGGKLEESKTLNTSEETI IDESDR-IRE-----RGI 14

82 PKPGDGQKIYEIDPTLKDFRSHLDYRYSEYRIRAI DQHEGGLA FSRGYEKLGFTRSA 14 QY

Db 142 PPPGLGQKIYEIDPLLTNTRQHLDRYSQYKKLRRAIDKYEGLAEAFSRGYEKMGFTRSA 20

142 EGITYREWAPGAHSALVGDFNNWNPNA^{DT}MTRDDYGVWEI^{FL}P^{NN}ADGSPAIPHGSRVK 20

Db 202 TGITYREWAPGAQSALIGDFNNWDANADIMTRNEFGVWEIFLPNNVDGSPAI PHGSRVK 26

QY 202 IRMDTPSGVKDISAWIKFSVQAPGEIPFNGIYYDPPEEEKVFQHPQPKRPESLRIYES 26

Db 262 IRMDTPSGVKDSIPAWINYSLQLPDEIPYNGIYYDPPEERYXFQHPRPCKPKSLRYES 322

QY 262 HIGMSSPEPKINSYANFRDEVLPRIKRLGYNVQIMAIQEHSSYASFQYHVTNFPAPSSR 32

Db 322 HIGMSSPEPKINSYVNERDEVLPRIKLGYNVAQIMAIQEHSYYASFQYHTVFAPSSR 38

QY 322 FGTPEDLKSLIDRAHEIGLLVLMDIVSHSSNNTLDGLNGFDGTDTHYFHGGPRGHMMW 38

D5 382 FGTPDDLKSLDKAHELGI VVLM DIVSHASNNTLDGLNMEDGTDSCYFHSGARGYHWMW 44

382 DSRLENYGSWEVLRFLLSNARWVLEEKFDGFRFDGVTSMYTHHGLQMTFTGNVEYFG 44

DB 442 DSRLEFNYGNWEVLRLLSNARWWLDEFKFDGFRPDGVTSMYTHHGLSVGPTGNYEEYFG 50

QY 442 FATDVDAVYLMVNDLIHGLHPDAVSIGEDVSGMPTFCIPVDPGGVGFDYRLHMAVADK 50

Db 502 LATDVDAVYLLMLVNDLIHGLFPDAITIGEDVSGMPTFCIPVQDGGVGFDYRLHMAIADK 56

QY 502 WIELKOSDESWMGDI VHTLTNRWLEKCVTYAESHDOALVGDKTIAFWLMDKDMYDFM 56

Db 562 WIELKKRDEDEDWRVGDIVHTLTNRWSEKCVSXAESHDAQALVGDKITAXWLMDKDMYDFM 62

562 ALDRPSTPRIDRGIALHKMIRLVITMGLGGEGLNFMGNFEGHPEWIDFPRGPOTLPTGKV 62

Db 622 ALDRPSTSLIDRGIALHKMIRLVTMGLGGEGYLNFMGNFEGHPEWIDFPRAEQHLSGVS 68

622 LPGNNSYDKRRFDLGDAFLRYHGMQEFDOAMOHLEEKYGFMTSEHQVSRKHEEDK 68

Db 682 IPGNQFSYDKCRRFDLGD AEYLRYHGLQEFDRAMQYLEDKYE FMTSEHQFISRKDEGDR 74

682 V I I F E R G D L V E V N F H M S N S F F D Y R V G C S R P G K Y K V A L D S D D A L F G G F S R L D H D V D Y F T T 74

Db 742 MIVFEXGNLVEFVNFHWTNSYS DYRIGCLKPGKYKVG LDDPLFGGFGRIDHNAEYFTS 80

QY 742 EHPHDNRPRSFVSYYTPSRTAVVYALTE 768

Db 802 EGSYDDRPXIMVYAPSRTAVVYALVD 828

РЕЗУЛТ 13

AAU80169
ID AAU80169 standard: protein: 849 AA

XX AC AAU80169;
 XX DT 15-JUL-2002 (first entry)
 XX DE Potato starch branching enzyme, SBE II.
 XX KM Potato; starch branching; enzyme; SBE II; glucan branching enzyme; GBE;
 XX KW plant; transgenic; antisense; food industry; paper industry;
 XX chemical industry.
 XX OS Solanum tuberosum.
 XX PN GH2360521-A.
 XX PD 26-SEP-2001.
 XX PF 20-MAR-2000; 2000GB-00006733.
 XX PR 20-MAR-2000; 2000GB-00006733.
 XX PI (DANI-) DANISCO AS.
 XX PI Poulsen P, Sorensen IS;
 XX DR WPI; 2001-650142/75.
 XX DR N-PSDE; ABK50301.
 XX PT New transformed plants with reduced endogenous starch branching enzyme
 PT and heterologous glucan branching enzyme activities, useful for producing
 PT starch with improved properties, which is in the food, paper and chemical
 PT industries.
 XX Example 1; Page 31-35; 61pp; English.
 XX PS
 XX CC The invention relates to a transformed organism, preferably a transformed
 CC plant, having a reduced endogenous starch branching enzyme (SBE)
 CC activity, and having a heterologous glucan branching enzyme (GBE)
 CC activity. The reduced SBE activity is effected via expression of a
 CC nucleotide sequence that is antisense to at least part of a SBE exon.
 CC Also included are a method of producing starch with altered
 CC characteristics comprising (a) providing a plant having reduced
 CC endogenous SBE activity, and having heterologous GBE activity (b)
 CC propagating the plant of (a) and optionally (c) obtaining starch from the
 CC plant; starch obtainable from the transformed plant; and a nucleic acid
 CC construct system capable of directing the expression of all or part of
 CC one or more antisense SBE exons and optionally one or more heterologous
 CC GBE. The transformed plants are useful for producing starch with modified
 CC and improved properties, which is an important raw material and used in
 CC the food, paper and chemical industries. The present sequence represents
 CC potato SBE II, used to make transgenic plants of the invention
 CC
 XX SQ Sequence 849 AA;
 SQ
 Query Match 76.7%; Score 3197; DB 4; Length 849;
 Best local similarity 72.6%; Pred. No. 4.5e-291;
 Matches 586; Conservative 82; Mismatches 91; Indels 48; Gaps 6;
 QY 2 ATFAVSGATL--GVAPPPAAAGPELQIPE-----DIEBQTAE----- 37
 DB 38 STVAASGKVLVGTGSDSSSSSTDDFEFETSPENSASTDVDSSTMEHASQIKTENDDV 97
 QY 38 ---VAMTGTAE-----KLESSEPTQGIIVETITGVTKGVEIVGEXRVV 81
 DB 98 EPSSDLTSSVEELDFASSIQLOEGGKLESKTLNFTFEETIDESDR-IRE-----RGI 149
 QY 82 PKPGDQGIYEIDPTIKDFRSHLDYRYSEYRIRAIRAIDQHEGGLAEFSRGYELGFTRSA 141
 DB 150 PPGGCGKIVIEDPLILNVRQHLDFYRSGYKRLRAIDYEGGLAEFSRGYELGFTRSA 209
 QY 142 EGIYREVAFGAAGALVGDFFNNKMPNATCTMRDDYGVWEIFLNNADGSPALPHSSRYK 201
 DB 210 TGIYREVAFGAAGALVGDFFNNKMPNATCTMRDDYGVWEIFLNNADGSPALPHSSRYK 269

QY 202 IMDTPSGVKDISAMIKFVQAPGEIPNGIYYDPEEEKYVFOHPQKRPESLR1YES 261
 DB 270 IMDTPSGVKDISAMINYSLOLPDEIPYNGIYYDPEEEKYVFOHRRPKPKSLRIYES 329
 QY 262 HIGMSSPEPKINSYANFDEVLPRIRLGNVAQVMAIQSHSYASGCHYTNFFAPSSR 321
 DB 330 HIGMSSPEPKINSYANFDEVLPRIRLGNVAQVMAIQSHSYASGCHYTNFFAPSSR 389
 QY 322 FGTPEDLKSLIDRAHGLGLVMDIVSHSSNNLTGLNFPDGDTHYFFGPGRGHMMW 381
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 QY 382 DRLFNYSQMEVLRFLISNARWMLBEEKFDPDGVTSMMYTHRGLQMTFTNGYGEYFG 441
 DB 450 DRLFNYSQMEVLRFLISNARWMLBEEKFDPDGVTSMMYTHRGLQMTFTNGYGEYFG 509
 QY 442 FATVDVAVVYLMVNDLHGLHDAVSIGEDVSGMPFCTIPEVDPGSGFPRRLMAVADK 501
 DB 510 LATVDVAVVYLMVNDLHGLHDAVSIGEDVSGMPFCTIPEVDPGSGFPRRLMAVADK 569
 QY 502 WTELKQSDSEWKGDIYHTITRRWLEKCVTAESHDOALYGDKTAFMLMDKMDYDM 561
 DB 570 WTELKQSDSEWKGDIYHTITRRWLEKCVTAESHDOALYGDKTAFMLMDKMDYDM 629
 QY 562 ALDRPSTPRIDRIGALHAKMIRLVTMGIGEGYINFMNGERGHPEWIDFPRGPOTLPFGKV 621
 DB 630 ALDRPSTPRIDRIGALHAKMIRLVTMGIGEGYINFMNGERGHPEWIDFPRGPOTLPFGKV 689
 QY 622 LPGNNSYDKCRRRPDLGADFLRHGMQFPDQMQHLEKYGMTSEHQVSKKHEBDK 681
 DB 690 IPGNQFSYDKCRRRPDLGADFLRHGMQFPDQMQHLEKYGMTSEHQVSKKHEBDK 749
 QY 682 VIFERGDIVFVNFPMNSFPDYRVGCSRPGKKVALLSDDALFGGFSRLHDHVDYFTT 741
 DB 750 VIFERGDIVFVNFPMNSFPDYRVGCSRPGKKVALLSDDALFGGFSRLHDHVDYFTT 809
 QY 742 EHPDNRPRSPSYTPSRITAVYALTE 768
 DB 810 EGMVDRPRSIMYVAPSRITAVYALTE 836
 RESULT 13
 AAM19113
 ID AAM19113 standard; protein; 878 AA.
 AC AAM19113;
 XX 26-AUG-1997 (first entry)
 DT
 XX
 XX Potato starch branching enzyme II.
 DE
 XX
 XX Starch branching enzyme II; bell gene; potato; transgenic plant;
 KW amylopectin; amylose; starch.
 XX
 XX Solanum tuberosum.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..48
 FT /label= Sig_peptide
 FT Misc-difference 33
 FT /note= "residue 33 was not detcd. owing to degeneracy of
 FT coding sequence (codon NTT)"
 FT Protein 49..878
 FT /label= Mat_protein
 FT Misc-difference 406
 FT /note= "residue 406 was not detcd. owing to degeneracy of
 FT coding sequence (codon TTN)"
 FT Misc-difference 570
 FT /note= "residue 570 was not detcd. owing to degeneracy of
 FT coding sequence (codon TNT)"
 XX
 XX W09720040-A1.

XX 05-JUN-1997. 96WO-SE001558.
 XX 28-NOV-1996; 96WO-SE001558.
 XX 29-NOV-1995; 95SE-00004272.
 XX 19-APR-1996; 96SE-00001506.
 XX (AMYL-) AMYLOGENE HB.
 XX Ek B, Khosnoodi J, Larsson C, Larsson H, Raek L;
 XX WPI, 1997-310596/28.
 XX N-PSDB; AAT69587.
 XX Isolated potato starch branching enzyme II - useful for altering degree
 XX of amylopectin branching and amylopectin/amylose ratio in potato starch.
 XX Claim 1; Page 12-15; 24pp; English.
 CC The amino acid sequence (AAW19113) for potato starch branching enzyme II
 CC (BEII) was deduced from a cDNA clone (AAT69587) isolated from tuber cDNA
 CC using primers (AAT69588-89) based on BEII tryptic peptides. It shows 68%
 CC identity to potato starch branching enzyme I and about 80% identity to
 CC BEII from other plant species. BEII, or functional active parts of the
 CC enzyme, can be expressed in transgenic potatoes. The starch obtd. from
 CC such plants will show a changed pattern of amylopectin branching and an
 CC altered amylopectin to amylose ratio
 CC
 XX Sequence 878 AA;

Query Match 76.6%; Score 3193; DB 2; Length 878;
 Best Local Similarity 72.6%; Pred. No. 1,1e-290;
 Matches 586; Conservative 82; Mismatches 91; Indels 48; Gaps 6;

QY 2 ATEAVSGATL--GVAPPPAAQPEELQIP-----DIEQQLAE----- 37
 DB 60 STVAASGKVLVPQTQSSSSSTQPEFTETSPENSPASTDVDSSTWEHASQIKTENDV 119
 QY 38 ---VAMTGTAE-----KLESEPTQGIIVETITDGTGKVELVGEKPRV 81
 DB 120 EPPSSDLTGSVEELDPASSLQLOEGGKLESTKLTNTSETITDESDR-IRF-----RGI 171
 QY 82 PKRGDQKIVEIDPTLKDFRSHLDYRYSEYRIRAPAIIDHGGLEAFSGYEKLGFTRSA 141
 DB 172 PPGGLGQKIYEIDPLLTNYQHLDYRSQYKLEALDKYEGGLEAFSGYEKMGFTRSA 231
 QY 142 EGTTYREMAFGAASALVDPNNNNPNADITMTDDYGVWETFLNNADGSAIIFHGSVYK 201
 DB 232 TGITTYREMAFGAASALVDPNNNNPNADITMTDDYGVWETFLNNADGSAIIFHGSVYK 291
 QY 202 IRMDTSGVVDSTISAWTKESVQAGEIPFNGIYVDPPEEEKYVPOHPKPKESRIYES 261
 DB 292 IRMDTSGVVDSTISAWTKESVQAGEIPFNGIYVDPPEEEKYVPOHPKPKESRIYES 351
 QY 262 HIGMSSPEPKINSYANFRDEVLPRIKELGYNAVOIMAIQHSYVAFSGYHVTNFFAPSSR 321
 DB 352 HIGMSSPEPKINSYANFRDEVLPRIKELGYNAVOIMAIQHSYVAFSGYHVTNFFAPSSR 411
 QY 322 FGTPEDLKSLIDRAHEIGLVMDIVSHSGNNLTLDGNGDGTDTYFHGGPRGHMMW 381
 DB 412 FGTPEDLKSLIDRAHEIGLVMDIVSHSGNNLTLDGNGDGTDTYFHGGPRGHMMW 471
 QY 382 DSRLEFNYSVGEVRLFLSNARWLEEKPFDPFGVTSMMYTHHGLQMTFTGNGEYFG 441
 DB 472 DSRLEFNYSVGEVRLFLSNARWLEEKPFDPFGVTSMMYTHHGLQMTFTGNGEYFG 531
 QY 442 FATDVAVVYVLMVNDLIHGLHPDAVSIIGEDVSGMPTFCIPVDPGVGFYRLMAVADK 501
 DB 532 LATDVAVVYVLMVNDLIHGLHPDAVSIIGEDVSGMPTFCIPVDPGVGFYRLMAVADK 591

DB 592 WIELKKRDEDMRVGDIIVHTLTNRWSEKCVSYAESHDQALVGDKTIAFWLMDKMYDFM 651
 QY 562 ALDRPSTPRIDRGIALHRIYLVMTGLGEGYLTINMGNEFGHPENIDFPRGQTLPTGYK 621
 DB 652 ALDRPSTSLIDRGIALHRIYLVMTGLGEGYLTINMGNEFGHPENIDFPRGQTLPTGYK 711
 QY 622 LFGNNNSYDKCRFPEDLDGADFLRYHGOEFPQAOHLEEKYGFMTSEHQYVSRKHEBDK 681
 DB 712 IPGNQFSTDKCRFPEDLDGADFLRYHGOEFPQAOHLEEKYGFMTSEHQYVSRKHEBDK 771
 QY 682 VIFERGLVFEVFNHWNSEFPDYRVGCSRFPGKYVVALDSDDALFGGSRDLHDVYFTT 741
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 QY 742 EHPHDPSPSPSVTPSRVAVYALTE 768
 DB 832 EGMVDDRPBSIMVYAPSRVAVYALVD 858

RESULT 14

AAW06400
 ID AAW06400 standard; protein; 847 AA.

XX AAW06400;

XX 25-FEB-1997 (first entry)

XX Class A starch branching enzyme (psbe2con.seq - clone psj30).

XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;

XX amylose; viscosity; potato.

XX Solanum tuberosum.

XX Key Location/Qualifiers

XX Peptide 1..11

XX Protein /label= sig_peptide

XX /label= mat_protein

XX W09634968-A2.

XX 07-NOV-1996.

XX 03-MAY-1996; 96WO-GB001075.

XX 05-MAY-1995; 95GB-00009229.

XX 10-APR-1996; 96GB-00007409.

XX (MAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;

XX Slidobottom CM, Westcott RJ;

XX WPI, 1996-506170/50.

XX N-PSDB; AAT42631.

XX New potato plant starch having high amylose content - also class A starch

XX branching enzyme and corresp. DNA to alter the viscosity of starch; for

XX use in food, biodegradable products, adhesives, etc.

XX Disclosure; Fig 12; 142pp; English.

XX Class A starch branching enzyme (SBE) has been obtained from potatoes. In

XX class A SBE mols., a flexible N-terminal domain, is found, which is not

XX found in class B mols

XX Sequence 847 AA;

Query Match 76.5%; Score 3189; DB 2; Length 847;
 Best Local Similarity 72.5%; Pred. No. 2,5e-290;
 Matches 585; Conservative 80; Mismatches 94; Indels 48; Gaps 6;

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QY 2 ATRAVSGATL--GVANPRPAAQPEELOIPF-----DIEQOTAE----- 37
DB 26 STVAAAGKVLVPGTQSDSSSSSTNQFFETSPENSPASTDVSSTVEMASQITENDDV 85
QY 38 ---VNMGTGTAEE-----KLESSEPTQGIYETITDQYTKGVKEIVGEXKRVV 81
DB 86 EPRSDLTGSVEILDPAFSLQLOEGCKLEESKTLTSETIIDESDR-IRE-----RGI 137
QY 82 PKFGDQKIYEIDPTLKDFRSHLDYRSEYRRIALADQHEGGLAERSRGKEKIGFTTSA 141
DB 138 PEPGLQCKIYEIDPLTNTYRQHLDYRYSQYKLEADIKKGGGLEAFSGYKMGFTTSA 197
QY 142 EGIITTEWAGASAAALVGDENNPNADMTWTRDQYWEI.FLPNNADGSPALPHGSRYK 201
DB 198 TGIITTEWAGAAQALIGDNNMDANADWTNBSFGWEL.FLPNNVDSFALPHGSRYK 257
QY 202 IRMDTPSGVDSISAWIKFSYQAPGEIPENGIVYDPPEEEKYVFOHPQKRESIRIYES 261
DB 258 IRMDTPSGVDSIPAWINYSQLPDEIPYNGIYDPEEEKRYIFQHPKPKPKSLRIYES 317
QY 262 HIGMSSEPKINSYANFRDEVLPRIKOLGYNVQIMAIQEHSYASFGIHYTNPFAPBSR 321
DB 318 HIGMSSEPKINSYANFRDEVLPRIKOLGYNVQIMAIQEHSYASFGIHYTNPFAPBSR 377
QY 322 FGRPDILKSLIDRAHEGLVLMIVSHSSGNTLDGLNGFDGPTDTHFHGQPRGHMMW 381
DB 378 FGRPDILKSLIDRAHEGLVLMIVSHSSGNTLDGLNGFDGPTDTHFHGQPRGHMMW 437
QY 382 DSRLFNYSWEVLRFLLSNARWMLZEYKFDGFRDGYTSMYTHHGLQMTFTGNYGEYFG 441
DB 438 DSRLFNYSWEVLRFLLSNARWMLDEYKFDGFRDGYTSMYTHHGLQMTFTGNYGEYFG 497
QY 442 FATDVDAVYLMVNDLHGHAPRAVSTIGEDVSGMPTFCIVPPDGVGFDRILNAVADK 501
DB 498 IATDVDAVYLMVNDLHGHAPRAVSTIGEDVSGMPTFCIVPPDGVGFDRILNAVADK 557
QY 502 WIELKXSDSKWKGDIVHTLTNRWLEKCVYAESHDQALVGDKTIAFWLMDKMYDFM 561
DB 558 WIELKXSDSKWKGDIVHTLTNRWLEKCVYAESHDQALVGDKTIAFWLMDKMYDFM 617
QY 562 ALDRPSTPRIDRGIALHMRILVMTGLGEGYLMNGNEFGHPENIDPPRGPTLPTGYK 621
DB 618 ALDRPSTPRIDRGIALHMRILVMTGLGEGYLMNGNEFGHPENIDPPRGPTLPTGYK 677
QY 622 LPGNNNSYDKRRPFDLGDADFLRYHGMQEPDQAMQHLEBKYGFTSEHQYVSRGHEEDK 681
DB 678 LPGNNNSYDKRRPFDLGDADFLRYHGMQEPDQAMQHLEBKYGFTSEHQYVSRGHEEDK 737
QY 682 VTIERDGLVFNFMHNSPFDYRVGSRPGKYVALDSDPALFGFSRLDHDVFTT 741
DB 738 VTIERDGLVFNFMHNSPFDYRVGSRPGKYVALDSDPALFGFSRLDHDVFTT 797
QY 742 EHPDNRPRSPSYTTPSRATVYALTE 768
DB 798 EHWYDNRPRSIMVYAPCRATVYALVD 824

RESULT 15
AAC39092
ID AAC39092 standard; protein; 858 AA.
XX
AC AAC39092;
XX
XX 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48321.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana
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Qy	263	IGMSSPEPKINSYANFRDEVLPRIKRLGYNVQIQAIOCHSYASFGYHVTNFFABSSRF 322
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Qy	323	GTPEDKLIDRAHGLGLVLTMDIVSHSSNNTLDGLNGFDGTDTHYFFHGGPRGHHMMD 382
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Qy	383	SRLFYGSWEVYLRFLTNSARWMLBKYKPGDFPDGTSMMWYTHGLQMTPTGNYGVEFGF 442
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QY 623 PGNNNSYDKCRRRPDLGDADFLRYHGMQEPDQAMQHEKYGFTSEHQYISRKHEGKV 682
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DB 693 AGNNGSYDKCRRRPDLGDADFLRYHGMQEPDQAMQHEKYGFTSEHQYISRKHEGKV 752
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 683 IIFRGDLVFYFNFWMSNSFPDYRVGCSRPGKYKVALDSDDALFGGFSRLDHDVDYFTTE 742
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DB 753 IIFRGDLVFYFNFWMSNSFPDYRVGCSRPGKYKVALDSDDALFGGFSRLDHDVDYFTTE 812
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OW protein - protein search, using sw model

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Title: US-09-508-377-12
Perfect score: 4169
Sequence: 1 MATFAVSGATLCAAPPAA.....PMSFVTPSTRAVVALTE 768

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCITUS.COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3915	93.9	729	4	US-09-609-040-4
2	3588.5	86.1	814	4	US-09-731-166-10
3	3351	80.2	799	4	US-09-731-166-12
4	3342	80.2	799	3	US-08-941-445A-15
5	3175	76.2	878	3	US-09-087-277-2
6	3175	76.2	878	4	US-09-658-499-2
7	2213	53.1	444	3	US-09-087
8	2213	53.1	444	4	US-08-658-489-4
9	2156.5	51.7	906	4	US-09-367-895-41
10	2146	51.5	822	3	US-08-941-445A-17
11	2146	51.5	822	4	US-09-731-166-14
12	1608	38.6	566	4	US-08-104-158-2
13	1608	38.6	566	4	US-09-609-040-2
14	576	13.8	762	4	US-09-579-365-2
15	541.5	13.0	762	4	US-09-537-120-2
16	538	12.9	681	4	US-09-489-039A-1131
17	535	12.8	823	4	US-09-252-991A-24768
18	528	12.7	652	4	US-08-528-026C-4
19	491.5	11.8	722	4	US-09-198-452A-513
20	297	7.1	648	4	US-09-252-991A-24668
21	282.5	6.8	559	3	US-08-242-680A-15
22	282.5	6.8	559	4	US-09-298-924-6
23	282.5	6.8	559	4	US-09-908-855-15
24	279	6.7	1938	4	US-09-514-302-2
25	276.5	6.6	893	4	US-09-514-302-4
26	267.5	6.4	793	4	US-09-463-238-5
27	253.5	6.1	606	3	US-09-187-124-2

28	253.5	6.1	606	4	US-09-850-936-2	Sequence 2, Appl
29	246	5.9	829	4	US-09-514-559-6	Sequence 6, Appl
30	246	5.9	862	3	US-09-346-237-1	Sequence 1, Appl
31	241.5	5.8	740	4	US-08-410-784A-4	Sequence 1, Appl
32	240	5.8	838	4	US-09-463-238-14	Sequence 14, Appl
33	237.5	5.7	789	4	US-09-731-166-16	Sequence 16, Appl
34	236.5	5.7	818	2	US-08-410-784A-2	Sequence 2, Appl
35	236.5	5.7	818	3	US-09-346-237-11	Sequence 11, Appl
36	233	5.6	589	1	US-08-399-646-2	Sequence 2, Appl
37	233	5.6	589	1	US-08-607-321-2	Sequence 2, Appl
38	233	5.6	589	2	US-08-607-321-2	Sequence 2, Appl
39	233	5.6	589	2	US-08-605-501-2	Sequence 2, Appl
40	233	5.6	596	1	US-08-399-646-12	Sequence 12, Appl
41	233	5.6	596	1	US-08-607-321-12	Sequence 12, Appl
42	233	5.6	596	2	US-08-961-240-12	Sequence 12, Appl
43	233	5.6	596	2	US-08-605-501-12	Sequence 12, Appl
44	230	5.5	597	1	US-08-399-646-4	Sequence 4, Appl
45	230	5.5	597	1	US-08-607-321-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1									
US-09-609-040-4									
Sequence 4, Application US/09609040									
Patent No. 6570066									
GENERAL INFORMATION:									
APPLICANT: Willmetter, et al.									
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT									
FILE REFERENCE: 51413-3515.1									
CURRENT FILING DATE: 2000-06-30									
PRIOR APPLICATION NUMBER: PCT/EP92/00302									
PRIOR FILING DATE: 1992-02-11									
NUMBER OF SEQ ID NOS: 4									
SOFTWARE: PatentIn version 3.0									
SEQ ID NO 4									
LENGTH: 729									
TYPE: PRT									
ORGANISM: Triticum aestivum									
US-09-609-040-4									
Query Match									
Best Local Similarity 93.9%; Score 3915; DB 4; Length 729;									
Matches 716; Conservative 98.2%; Pred. No. 0;									
Mismatches 6; Indels 0; Gaps 0;									
QY	40	MTGTAKEKLESEPTQGIYETITTDGTVKVKELVNGEKPRVYKPGDGCKIYEIDPLKD	99						
DB	1	MTGTAKEKLESEPTQGIYETITTDGTVKVKELVNGEKPRVYKPGDGCKIYEIDPLKD	60						
QY	100	FSHLDYRSEYRRIKRAIDQHEGGLAERSRGYKLGFTSAEGITREMAFGAHSALV	159						
DB	61	FSHLDYRSEYRRIKRAIDQHEGGLAERSRGYKLGFTSAEGITREMAFGAHSALV	120						
QY	160	GDFFNNPNDATMDTDYGVWEIPLFNNDGSPALPHGSRVYKTRMDTPSGVKSISAWIK	219						
DB	121	GDFFNNPNDATMDTDYGVWEIPLFNNDGSPALPHGSRVYKTRMDTPSGVKSISAWIK	180						
QY	220	FEVQAPGEIPNGIYDPEEKEVYVHOHQPESELRITYESHIGMSPEPKINSYANFR	279						
DB	181	FEVQAPGEIPNGIYDPEEKEVYVHOHQPESELRITYESHIGMSPEPKINSYANFR	240						
QY	280	DEVLPRIKELGVNAVOINAIQHSYVAFGYHTNFPAPSRGTPEDLSLIDRAHELG	339						
DB	241	DEVLPRIKELGVNAVOINAIQHSYVAFGYHTNFPAPSRGTPEDLSLIDRAHELG	300						
QY	340	LIVLMDIVSHSSNNTLDLNGFDGTDTHYFHGCGPGHMMMSRLFNYSWEVLRFLLS	399						
DB	301	LIVLMDIVSHSSNNTLDLNGFDGTDTHYFHGCGPGHMMMSRLFNYSWEVLRFLLS	360						
QY	400	NARWMLIEVKPFGFRDGVTSMMVYTHGLQMTFTGVYGEYFGFATDVAVYVLMVNDLI	459						

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Db      361 NAWMVEEVDFGRFDGVTSMWYTHHGLQWTFNGYGEYGFATDVDAVYVLMVNDLI 420
QY      460 HGHAPDAVSGEDVSGMPTFCIPVDPGVGFVDRHLHNAVADKMTIELLKQSDSMKMGDIY 519
Db      421 HGLYPAVSGEDVSGMPTFCIPVDPGVGFVDRHLHNAVADKMTIELLKQSDSMKMGDIY 480
QY      520 HTLNBRWLEKCVTYAASHQALVGDKTIAFWLMDKMDYEMALDRPSTPRIDRGIALHK 579
Db      481 HTLNBRWLEKCVTYAASHQALVGDKTIAFWLMDKMDYEMALDRPSTPRIDRGIALHK 540
QY      580 MRLVTWGLGEGYLNFMGNEFGHPWIDPFRGPQTLPTGKVLPGNNNSYDKCRRRFDLG 639
Db      541 MRLVTWGLGEGYLNFMGNEFGHPWIDPFRGPQTLPTGKVLPGNNNSYDKCRRRFDLG 600
QY      640 DADPLRHGQEFQOAMQHLBEKYGFMTSSEHOYYSRKHEEDKVIIFEEGDLVFNFMHMS 699
Db      601 DAEFLRYRGMQEFQOAMQHLBEKYGFMTSSEHOYYSRKHEEDKVIIFEEGDLVFNFMHMS 660
QY      700 NSFEDYVGSRGPKYKVALDSDDALFGFSRLDHDVDYFTTEHPHNDRPRSFSYVTPSR 759
Db      661 NSFEDYVGSRGPKYKVALDSDDALFGFSRLDHDVDYFTTEHPHNDRPRSFSYVTPSR 720
QY      760 TAVVYALTE 768
Db      721 TAVVYALTE 729

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RESULT 2
US-09-731-166-10
; Sequence 10, Application US/09731166
; Patent No. 6639126
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccarides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731,166
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,993
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 814
; TYPE: PRT
; ORGANISM: Zea mays
US-09-731-166-10

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Query Match      86.1%; Score 3588.5; DB 4; Length 814;
Best Local Similarity 84.7%; Pred. No. 0;
Matches 662; Conservative 32; Mismatches 49; Indels 39; Gaps 4;

QY      11 LGVAPPPAAQPEELQIPEDIEBQTAENVMTGTAKLESSEPTQ----- 55
Db      38 LLSAEPVVDQTQPEELQIPEDIEBQTAENVMTGTAKLESSEPTQ----- 85
QY      56 -----GIYETITDGVTKGKELVGEKPRVVPKPGGQKIYEIDPTLKDPRSH 103
Db      86 ERPELSEVIGVGGTGKTIDGAKAKADLVBEKPRVLPDPGGQKIYEIDPTLKBGRGH 145
QY      104 LDYRSEYRRIARAIDQHEGGLAEAFSGYEKLGFTSASGITYREMAPGASHAALVGDEN 163
Db      146 LDYRSEYRRIARAIDQHEGGLAEAFSGYEKLGFTSASGITYREMAPGASHAALVGDEN 205
QY      164 NNNPNADVTMDQDYGWEIFLNNADGSPALIPHGSVYKTRMDTPSGVKSISWITFSVQ 223
Db      206 NNNPNADVTMDQDYGWEIFLNNADGSPALIPHGSVYKTRMDTPSGVKSISWITFSVQ 265
QY      224 APGEIPEKGIYVDPPEEKYVFOHPQKRPESLRITYESHIGMSPEPKINSYANFDEVL 283
Db      266 APGEIPEKGIYVDPPEEKYVFOHPQKRPESLRITYESHIGMSPEPKINSYANFDEVL 325

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QY      284 PRKLGYNVAOIMAIQESHYSYASFGRYHTNFFAPSSRGCTPEDKSLIDRAHELGILV 343
Db      326 PRKLGYNVAOIMAIQESHYSYASFGRYHTNFFAPSSRGCTPEDKSLIDRAHELGILV 385
QY      344 MDIVASHSSNNLTLDGNGFDGTDTYHFGGPRGHHMMMSRLFNYSWEYLRFLSNARW 403
Db      386 MDIVASHSSNNLTLDGNGFDGTDTYHFGGPRGHHMMMSRLFNYSWEYLRFLSNARW 445
QY      404 WLEEKYFDGFRPDGVTSMWYTHHGLQWTFNGYGEYGFATDVDAVYVLMVNDLIHGLH 463
Db      446 WLEEKYFDGFRPDGVTSMWYTHHGLQWTFNGYGEYGFATDVDAVYVLMVNDLIHGLH 505
QY      464 PDVSGIEDVSGMPTFCIPVDPGVGFVDRHLHNAVADKMTIELLKQSDSMKMGDIYHLLT 523
Db      506 PDVSGIEDVSGMPTFCIPVDPGVGFVDRHLHNAVADKMTIELLKQSDSMKMGDIYHLLT 565
QY      524 NRRWLEKCVTYAASHQALVGDKTIAFWLMDKMDYEMALDRPSTPRIDRGIALHKMIRL 583
Db      566 NRRWLEKCVTYAASHQALVGDKTIAFWLMDKMDYEMALDRPSTPRIDRGIALHKMIRL 625
QY      584 VTMGLGEGYLNFMGNEFGHPWIDPFRGPQTLPTGKVLPGNNNSYDKCRRRFDLGADP 643
Db      626 VTMGLGEGYLNFMGNEFGHPWIDPFRGPQTLPTGKVLPGNNNSYDKCRRRFDLGADP 685
QY      644 LRYHGMQEFQOAMQHLBEKYGFMTSSEHOYYSRKHEEDKVIIFEEGDLVFNFMHMSFF 703
Db      686 LRYHGMQEFQOAMQHLBEKYGFMTSSEHOYYSRKHEEDKVIIFEEGDLVFNFMHMSFF 745
QY      704 DYRVGSGRGPKYKVALDSDDALFGFSRLDHDVDYFTTEHPHNDRPRSFSYVTPSRVAV 763
Db      746 DYRVGSGRGPKYKVALDSDDALFGFSRLDHDVDYFTTEHPHNDRPRSFSYVTPSRVAV 805
QY      764 YA 765
Db      806 YA 807

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RESULT 3
US-09-731-166-12
; Sequence 12, Application US/09731166
; Patent No. 6639126
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccarides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731,166
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,993
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Zea mays
US-09-731-166-12

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Query Match      80.4%; Score 3351; DB 4; Length 799;
Best Local Similarity 78.5%; Pred. No. 1,1e-309;
Matches 609; Conservative 68; Mismatches 77; Indels 22; Gaps 4;

QY      4 FAVSGATLGV-----APPAAQPEELQIPEDIEBQTAENVMTGTAKLESSE----- 52
Db      35 FLTRGARVVGSGTGHGARRAAARAAVAVPBGEND-----GLASRAASQAQOSDEL 85
QY      53 PLOGIYETITDGVTKGKELVGEKPRVVPKPGGQKIYEIDPTLKDPRSHLDYRSEYR 112
Db      86 EVDPISEETTCGA--GAADAQALNRVAVPPSPGQKIYQIDPMQGIKYLHEVYYSLYR 143
QY      113 RIRAAIDQHEGGLAEAFSGYEKLGFTSASGITYREMAPGASHAALVGDENNNPNADVTM 172
Db      144 RIRSDIDHEGGLAEAFSGYEKLGFTSASGITYREMAPGASHAALVGDENNNPNADVTM 203

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173 TRDYGWVEIFLPPNADGSPALPHGSRVXIRMDTPSGVKDSISAMTKFSVOAGGEIPFG 232
204 SKNEFGWVEIFLPPNADGSPALPHGSRVXIRMDTPSGIKDIPAMTKFSVOAGGEIPFG 263
223 IYDPEEKEKYVFOHPQRPSLRITYESHIGMSSEPKINSYANPDEVLPRIKLGYN 292
264 IYDPEEKEKYVFOHPQRPSLRITYESHIGMSSEPKINSYANPDEVLPRIKLGYN 323
293 AVOIMAIQESHYSYAFGYHVTNFPAPSSRFGTPEBILKSLIDRAHEGLVLMIVSHSS 352
324 AVOIMAIQESHYSYAFGYHVTNFPAPSSRFGTPEBILKSLIDRAHEGLVLMIVSHSS 383
353 NNTLDGLNGFDGTDTHYFHGGRPGHMMWDSRLFNNGSWVLAPFLSNAMWLEBYKQEF 412
384 SNTLDGLNGFDGTDTHYFHGGRPGHMMWDSRLFNNGSWVLAPFLSNAMWLEBYKQEF 443
413 PRFDGVTSMYTHHGLQMTFTNGYGEFGPATDVDAVVYLMVNDLHGLHAPVSIGED 472
444 PRFDGVTSMYTHHGLQMTFTNGYGEFGPATDVDAVVYLMVNDLHGLHAPVSIGED 503
473 VSGMPTFCIPVDDGVGFYRLHMAVADKMIELKOSDESMWKGDIVHTLTNRMLEKCV 532
504 VSGMPTFCIPVDDGVGFYRLHMAVADKMIELKOSDESMWKGDIVHTLTNRMLEKCV 563
533 TYAESHDQALVGDKTIAFWLMDKMDYDPMALDRPSTPTIDRGIALHMKIRLITWGLGEG 592
564 TYAESHDQALVGDKTIAFWLMDKMDYDPMALDRPSTPTIDRGIALHMKIRLITWGLGEG 623
593 YLNFPGNEFGHEWIDFPGPOTLPTGKYLPGNNNSYDKCRPRFDLGDADFLRYHGOEF 652
624 YLNFPGNEFGHEWIDFPGPOTLPTGKYLPGNNNSYDKCRPRFDLGDADFLRYHGOEF 683
653 DOAMQHEEKGFMTESEHQYVSRKHEEDKVIIFERGLVFEVFNHMSNPFYRVGCSR 712
684 DOAMQHEEKGFMTESEHQYVSRKHEEDKVIIFERGLVFEVFNHMSNPFYRVGCSR 743
713 GYKYVALDSDALFGGFSRLDHDVDYFTTBHNDNRPSFSVYTPSTAVVYALTE 768
744 GYKYVALDSDALFGGFSRLDHDVDYFTTBHNDNRPSFSVYTPSTAVVYALTE 799

RESULT 4
US-08-941-445A-15
Sequence 15, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
TITLE OF INVENTION: Scarth Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941.445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28 547

REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-941-445A-15
Query Match
80.2%; Score 3342; DB 3; Length 799;
Best Local Similarity 78.4%; Pred. No. 7,9e-309;
Matches 608; Conservative 67; Mismatches 79; Indels 22; Gaps 4;

4 FAVGATLGV-----ARPPAAQPEELQIPEDIEQTAENVNTGTAELKESSE----- 52
35 FLTRGARVCGSGTHGAMRAAAARAVMVEGEND-----GLASRADSAQFOSDEL 85
53 PTGCIIVETITGVTGKVELVGEKPRVVKRGDQKIVIEIDPTLDFSHLDYRSEYR 112
86 EVPIISEETTGA--GVADAQALNVRVPPPSDQKIFQIDPMQGYRHLBYRSLVR 143
113 RIRAIIDHEGGLAFAFSRGEKLGFTSAEGITTYREWAPGAHSAALVGFNNNNPNADTM 172
144 RIRSDIDHEGGLAFAFSRGEKGNASAEGITTYREWAPGAHSAALVGVNNNDPNADM 203
173 TRDDYGWVEIFLPPNADGSPALPHGSRVXIRMDTPSGVKDSISAMTKFSVOAGGEIPFG 232
204 SKNEFGWVEIFLPPNADGSPALPHGSRVXIRMDTPSGIKDIPAMTKFSVOAGGEIPFG 263
223 IYDPEEKEKYVFOHPQRPSLRITYESHIGMSSEPKINSYANPDEVLPRIKLGYN 292
264 IYDPEEKEKYVFOHPQRPSLRITYESHIGMSSEPKINSYANPDEVLPRIKLGYN 323
293 AVOIMAIQESHYSYAFGYHVTNFPAPSSRFGTPEBILKSLIDRAHEGLVLMIVSHSS 352
324 AVOIMAIQESHYSYAFGYHVTNFPAPSSRFGTPEBILKSLIDRAHEGLVLMIVSHSS 383
353 NNTLDGLNGFDGTDTHYFHGGRPGHMMWDSRLFNNGSWVLAPFLSNAMWLEBYKQEF 412
384 SNTLDGLNGFDGTDTHYFHGGRPGHMMWDSRLFNNGSWVLAPFLSNAMWLEBYKQEF 443
413 PRFDGVTSMYTHHGLQMTFTNGYGEFGPATDVDAVVYLMVNDLHGLHAPVSIGED 472
444 PRFDGVTSMYTHHGLQMTFTNGYGEFGPATDVDAVVYLMVNDLHGLHAPVSIGED 503
473 VSGMPTFCIPVDDGVGFYRLHMAVADKMIELKOSDESMWKGDIVHTLTNRMLEKCV 532
504 VSGMPTFCIPVDDGVGFYRLHMAVADKMIELKOSDESMWKGDIVHTLTNRMLEKCV 563
533 TYAESHDQALVGDKTIAFWLMDKMDYDPMALDRPSTPTIDRGIALHMKIRLITWGLGEG 592
564 TYAESHDQALVGDKTIAFWLMDKMDYDPMALDRPSTPTIDRGIALHMKIRLITWGLGEG 623
593 YLNFPGNEFGHEWIDFPGPOTLPTGKYLPGNNNSYDKCRPRFDLGDADFLRYHGOEF 652
624 YLNFPGNEFGHEWIDFPGPOTLPTGKYLPGNNNSYDKCRPRFDLGDADFLRYHGOEF 683
653 DOAMQHEEKGFMTESEHQYVSRKHEEDKVIIFERGLVFEVFNHMSNPFYRVGCSR 712
684 DOAMQHEEKGFMTESEHQYVSRKHEEDKVIIFERGLVFEVFNHMSNPFYRVGCSR 743
713 GYKYVALDSDALFGGFSRLDHDVDYFTTBHNDNRPSFSVYTPSTAVVYALTE 768
744 GYKYVALDSDALFGGFSRLDHDVDYFTTBHNDNRPSFSVYTPSTAVVYALTE 799

RESULT 5
US-09-087-277-2
Sequence 2, Application US/09087277B
Patent No. 6169226

```

GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 878
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism:be11 gene (branching enzyme II)
US-09-087-277-2

Query Match      76.2%; Score 3175; DB 3; Length 878;
Best Local Similarity 72.2%; Pred. No. 7.3e-293;
Matches 583; Conservative 83; Mismatches 93; Indels 48; Gaps 6;

QY 2 ATFAVSATL--GVARPPAAQPELOIP-----DIEQTAE----- 37
DB 60 STVAASGVLPQTQSSSSSTQFETSPENSASTVDVDSSTMHARQIKTENDV 119
QY 38 ---VNMTGTAE-----KLESSEPTQIGVETITDGYTKGKELVGEKPRV 81
DB 120 EPSDDLGSVEEDLFASSLQLEGKLESKLTNSETITIDESDR-IRE-----RGI 171
QY 82 PKPGDGQKIYEIDPTLKDPSHLDYRSEYRIRPAIDQHGGLAFBSRGYKLGFTSA 141
DB 172 PPGGLGQKIYEIDPLTNRYQHLDRYSQYKKEALDKYEGGLAFBSRGYKMGFTSA 231
QY 142 EGIITYREMAPGASAAALVGDFFNNMNPADMTTRDYGWEIFLPNNADGSPAIPIGSRV 201
DB 232 TGIITYREMAPGASAAALVGDFFNNMNPADMTTRDYGWEIFLPNNADGSPAIPIGSRV 291
QY 202 IRMDTPSGVXDSISAMIKFSVQAPGEIPFNGIYYDPPEBEKXYVQHPQKPEESLRIYES 261
DB 292 IRMDTPSGVXDSISAMIKFSVQAPGEIPFNGIYYDPPEBEKXYVQHPQKPEESLRIYES 351
QY 262 HIGMSSEPKINSYANFDEVLPRIKLGYNAAVOIMAOESHYASFGYHTNFPAPSSR 321
DB 352 HIGMSSEPKINSYANFDEVLPRIKLGYNAAVOIMAOESHYASFGYHTNFPAPSSR 411
QY 322 FGTPEEDLKSLLDRAHELGLVLMIVSHSSNNTLDGLNGFDGTDHYHGGPRGHMMW 381
DB 412 FGXEDDLKSLLDRAHELGLVLMIVSHSSNNTLDGLNGFDGTDHYHGGPRGHMMW 471
QY 382 DSRLEFNTGSEWEYLRLELGNARWMLLEEKDFGFRPDGVTSMTYTHGLQMTFTGNYGEYFG 441
DB 472 DSRLEFNTGSEWEYLRLELGNARWMLLEEKDFGFRPDGVTSMTYTHGLQMTFTGNYGEYFG 531
QY 442 FATVDVAVYITLTVNDLHGLHPDAVSTEDVSGMPTFCIPYPDGSGVDYRLHMAVAAR 501
DB 532 LATVDVAVYITLTVNDLHGLHPDAVSTEDVSGMPTFCIPYPDGSGVDYRLHMAVAAR 591
QY 502 MIELLKQDESQKMGDIYHTLTNRRLLEKCYTYAESHDQALVGDKTIATMLDKDXYDPM 561
DB 592 WIELKKKDEDEMRVGDYHTLTNRRLLEKCYTYAESHDQALVGDKTIATMLDKDXYDPM 651
QY 562 ALDRSEPRIDRGLALHXRIRLVTVNGLGEGYLNFNGNEFGHEWIDPPGPGTLEFGKY 621
DB 652 ALDRSEPRIDRGLALHXRIRLVTVNGLGEGYLNFNGNEFGHEWIDPPGPGTLEFGKY 711

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681 LPGNNSYDKCRRRFDLGDADFLRYHGMQFDOAMQHLSEKYGFMTESEHQYVSRKHEEDK
712 IPGNQFSTDKCRRRFDLGDADFLRYHGMQFDOAMQHLSEKYGFMTESEHQYVSRKHEEDK
771
QY 682 VIFERGLVFEVFNHWSNFPDYGCSRPFGKYVALDSDDALFGGFSRLDHDVDYFTT 741
DB 772 MIVFEGKLVFEVFNHWSNFPDYGCSRPFGKYVALDSDDALFGGFSRLDHDVDYFTT 831
QY 742 EHPHNRPSRSEVYTPSRATVYALTE 768
DB 832 EGMYDRRPSRIMVYAPSRATVYALVD 858

RESULT 6
US-09-658-499-2
Sequence 2, Application US/09658499
Patent No. 6469231
GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/658,499
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR FILING DATE: 1996-11-28
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 878
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism:be11 gene (branching enzyme II)
US-09-658-499-2

Query Match      76.2%; Score 3175; DB 4; Length 878;
Best Local Similarity 72.2%; Pred. No. 7.3e-293;
Matches 583; Conservative 83; Mismatches 93; Indels 48; Gaps 6;

QY 2 ATFAVSATL--GVARPPAAQPELOIP-----DIEQTAE----- 37
DB 60 STVAASGVLPQTQSSSSSTQFETSPENSASTVDVDSSTMHARQIKTENDV 119
QY 38 ---VNMTGTAE-----KLESSEPTQIGVETITDGYTKGKELVGEKPRV 81
DB 120 EPSDDLGSVEEDLFASSLQLEGKLESKLTNSETITIDESDR-IRE-----RGI 171
QY 82 PKPGDGQKIYEIDPTLKDPSHLDYRSEYRIRPAIDQHGGLAFBSRGYKLGFTSA 141
DB 172 PPGGLGQKIYEIDPLTNRYQHLDRYSQYKKEALDKYEGGLAFBSRGYKMGFTSA 231
QY 142 EGIITYREMAPGASAAALVGDFFNNMNPADMTTRDYGWEIFLPNNADGSPAIPIGSRV 201
DB 232 TGIITYREMAPGASAAALVGDFFNNMNPADMTTRDYGWEIFLPNNADGSPAIPIGSRV 291
QY 202 IRMDTPSGVXDSISAMIKFSVQAPGEIPFNGIYYDPPEBEKXYVQHPQKPEESLRIYES 261
DB 292 IRMDTPSGVXDSISAMIKFSVQAPGEIPFNGIYYDPPEBEKXYVQHPQKPEESLRIYES 351
QY 262 HIGMSSEPKINSYANFDEVLPRIKLGYNAAVOIMAOESHYASFGYHTNFPAPSSR 321
DB 352 HIGMSSEPKINSYANFDEVLPRIKLGYNAAVOIMAOESHYASFGYHTNFPAPSSR 411
QY 322 FGTPEEDLKSLLDRAHELGLVLMIVSHSSNNTLDGLNGFDGTDHYHGGPRGHMMW 381
DB 412 FGXEDDLKSLLDRAHELGLVLMIVSHSSNNTLDGLNGFDGTDHYHGGPRGHMMW 471
QY 382 DSRLEFNTGSEWEYLRLELGNARWMLLEEKDFGFRPDGVTSMTYTHGLQMTFTGNYGEYFG 441
DB 472 DSRLEFNTGSEWEYLRLELGNARWMLLEEKDFGFRPDGVTSMTYTHGLQMTFTGNYGEYFG 531
QY 442 FATVDVAVYITLTVNDLHGLHPDAVSTEDVSGMPTFCIPYPDGSGVDYRLHMAVAAR 501
DB 532 LATVDVAVYITLTVNDLHGLHPDAVSTEDVSGMPTFCIPYPDGSGVDYRLHMAVAAR 591
QY 502 MIELLKQDESQKMGDIYHTLTNRRLLEKCYTYAESHDQALVGDKTIATMLDKDXYDPM 561
DB 592 WIELKKKDEDEMRVGDYHTLTNRRLLEKCYTYAESHDQALVGDKTIATMLDKDXYDPM 651
QY 562 ALDRSEPRIDRGLALHXRIRLVTVNGLGEGYLNFNGNEFGHEWIDPPGPGTLEFGKY 621
DB 652 ALDRSEPRIDRGLALHXRIRLVTVNGLGEGYLNFNGNEFGHEWIDPPGPGTLEFGKY 711

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Db 352 HIGMSPEPKINSYVNFDEVLPRIKLGYNVQIMAIQESHYASFGYHNTFXAPESR 411
QY 322 FGTPEDLKSLIDRAHELGILVLMDIVSHSSNNTLDGLNGFDGDTYHFGPGRGHMMW 381
Db 412 FGAPDULKSLIDKAHELGIYVLMDIVSHSSNNTLDGLNMFDDGDSYCFHSGANGYHMMW 471
QY 382 DSRLEFYNGWEVLRFLISNARWMLBEKFFDGFDTSMYTYHGLQMTTGNYGEYFG 441
Db 472 DSRLEFYNGWEVLRFLISNARWMLBEKFFDGFDTSMYTYHGLQMTTGNYGEYFG 531
QY 442 FARDVAVAVYVLMVNDLHGLHPDAVSIAGEDVSGMPTFCIPVPGGVGFDYRLHNAVADK 501
Db 532 LATDVDAVYVLMVNDLHGLHPDAVSIAGEDVSGMPTFCIPVPGGVGFDYRLHNAVADK 591
QY 502 WIELLKOSDESWMKGDIVHTLTNRWLEKCYTVAESHDOALVGDXTIAFWLMDKMDYDFM 561
Db 592 WIELLKRDDEDMRGDIVHTLTNRWSEKCYVAESHDOALVGDXTIAFWLMEKMDYDFM 651
QY 562 ALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLMFMGNEFGHPEWIDPRBPOTLPYGV 621
Db 652 ALDRXSTSLADRGIALHKMIRLVTMGLGEGYLMFMGNEFGHPEWIDPRBPOTLPYGV 711
QY 622 LPGNNNSYDCRRRFDGADFLRYHGMQEPDQAMOHLEEKYGFMTSEHOVSRKHEEDK 681
Db 712 LPGNNNSYDCRRRFDGADFLRYHGMQEPDQAMOHLEEKYGFMTSEHOVSRKHEEDK 771
QY 682 VIFERGDVLFVENFHMNSGFDDYRVCSPRGYKVALSDDALFGFSRLDHDVYFTT 741
Db 772 MIVFEKGNLVFVFNFMHTKSYSDYRICGLKRGYKVALSDDALFGFSRLDHDVYFTT 831
QY 742 EHPHDKRPSFSYTTBRTAVYALTE 768
Db 832 EGMVDDRPSIMYVAPSRITAVYALVD 858

RESULT 7
US/09/087
/ Sequence 4, Application US/09087277B
/ Patent No. 6169226
/ GENERAL INFORMATION:
/ APPLICANT: EK, Bo
/ APPLICANT: KHOSNODI, Jamehid
/ APPLICANT: LARSSON, Clas-Tomas
/ APPLICANT: RASK, Lars
/ TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
/ FILE REFERENCE: 003300-486
/ CURRENT APPLICATION NUMBER: US/09/087, 277B
/ PRIOR FILING DATE: 1998-05-29
/ EARLIER APPLICATION NUMBER: PCT/SE96/01558
/ EARLIER FILING DATE: 1996-11-28
/ EARLIER APPLICATION NUMBER: SE 9504272-7
/ EARLIER FILING DATE: 1995-11-29
/ EARLIER APPLICATION NUMBER: SE 9601506-0
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 464
/ TYPE: PRF
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism:be11 gene fragment (branching enz
US/09/087,277-4

Query Match 53.1%; Score 2213; DB 3; Length 464;
Best Local Similarity 86.0%; Pred. No. 9.3e-202;
Matches 398; Conservative 31; Mismatches 34; Indels 0; Gaps 0;
QY 184 LPMNADGSPAIPIHSGRYKIRMDTPSGVSDSISAMIKFSVQAPGELPFNGIYDPEEERY 243
Db 1 LPMNVDGSPAIPIHSGRYKIRMDTPSGVSDSISAMIKFSVQAPGELPFNGIYDPEEERY 60

QY 244 VQHPQPKPESLRITYESHIGMSSPEPKINSYANFRDEVLPRIKLGYNVQIMAIQESH 303
Db 61 IFQHPRPKPKSLRIYESHIGMSSPEPKINSYANFRDEVLPRIKLGYNVQIMAIQESH 120
QY 304 YVASFGYHNTNFAPSPRFGTPEDLKSLIDRAHELGILVLMDIVSHSSNNTLDGLNGFD 363
Db 121 YVASFGYHNTNFAPSPRFGTPEDLKSLIDRAHELGILVLMDIVSHSSNNTLDGLNGFD 180
QY 364 GTDTHYFHGPRGHHMMWDSRLFNYSWEVLRFLISNARWMLBEKFFDGFDTSMY 423
Db 181 GDSYCFHSGANGYHMMWDSRLFNYSWEVLRFLISNARWMLBEKFFDGFDTSMY 240
QY 424 THHGQMTTGNYGEYFGATDVAVYVLMVNDLHGLHPDAVSIAGEDVSGMPTFCIPV 483
Db 241 THHGQMTTGNYGEYFGATDVAVYVLMVNDLHGLHPDAVSIAGEDVSGMPTFCIPV 300
QY 484 PDGVGFDYRLHNAVADKIELLKOSDESWMKGDIVHTLTNRWLEKCYTVAESHDOALV 543
Db 301 QDGVGFDYRLHNAVADKIELLKOSDESWMKGDIVHTLTNRWSEKCYVAESHDOALV 360
QY 544 GDXTIAFWLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLMFMGNEFGH 603
Db 361 GDXTIAFWLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLMFMGNEFGH 420
QY 604 PEWIDPRBPOTLPYGVLPNNNSYDCRRRFDGADFLRY 646
Db 421 PEWIDPRBPOTLPYGVLPNNNSYDCRRRFDGADFLRY 463

RESULT 8
US-09-658-499-4
/ Sequence 4, Application US/09658499
/ Patent No. 6469231
/ GENERAL INFORMATION:
/ APPLICANT: EK, Bo
/ APPLICANT: KHOSNODI, Jamehid
/ APPLICANT: LARSSON, Clas-Tomas
/ APPLICANT: RASK, Lars
/ TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
/ FILE REFERENCE: 003300-486
/ CURRENT APPLICATION NUMBER: US/09/658, 499
/ PRIOR FILING DATE: 2000-09-08
/ PRIOR APPLICATION NUMBER: 09/087, 277
/ PRIOR FILING DATE: 1998-05-29
/ PRIOR APPLICATION NUMBER: PCT/SE96/01558
/ PRIOR FILING DATE: 1996-11-28
/ PRIOR APPLICATION NUMBER: SE 9504272-7
/ PRIOR FILING DATE: 1995-11-29
/ PRIOR APPLICATION NUMBER: SE 9601506-0
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 464
/ TYPE: PRF
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism:be11 gene fragment (branching en
US-09-658-499-4

Query Match 53.1%; Score 2213; DB 4; Length 464;
Best Local Similarity 86.0%; Pred. No. 9.3e-202;
Matches 398; Conservative 31; Mismatches 34; Indels 0; Gaps 0;
QY 184 LPMNADGSPAIPIHSGRYKIRMDTPSGVSDSISAMIKFSVQAPGELPFNGIYDPEEERY 243
Db 1 LPMNVDGSPAIPIHSGRYKIRMDTPSGVSDSISAMIKFSVQAPGELPFNGIYDPEEERY 60
QY 244 VQHPQPKPESLRITYESHIGMSSPEPKINSYANFRDEVLPRIKLGYNVQIMAIQESH 303
Db 61 IFQHPRPKPKSLRIYESHIGMSSPEPKINSYANFRDEVLPRIKLGYNVQIMAIQESH 120

QY 304 YVAFYGVHTNFPAPSSRFCTPEDLKLSDRAHEGLLVNDIVHSHSNNTLDGNGPD 363
 DB 121 YVAFYGVHTNFPAPSSRFCTPEDLKLSDRAHEGLLVNDIVHSHSNNTLDGNGPD 180
 QY 364 GTDTHYHGGGRHHMMWDSRLFNYSGVSWVTRFLISNARWMLLEEKFGFRDGYTSMMY 423
 DB 181 GTDSCFHSYGARGYHMMWDSRLFNYSGVSWVTRFLISNARWMLLEEKFGFRDGYTSMMY 240
 QY 424 THHLOMTFNGNVEYEGFATDVAVVYLMVNDLHGLHPDASIGEDVSGMPTFCIPV 483
 DB 241 THHLSVSGFTNYSYEGFATDVAVVYLMVNDLHGLHPDASIGEDVSGMPTFCIPV 300
 QY 484 PDGSGVGFYRLHMAVADKMIELKQSDSWKMGDIVHTLTNRNMLEKCVTAESHDOALV 543
 DB 301 QDGGVGFYRLHMAVADKMIELKQSDSWKMGDIVHTLTNRNMLEKCVTAESHDOALV 360
 QY 544 GDKTIAFWLMDKMDYDFMALDPSPTPRIDRGIALHKTMLVMTGIGSGYLNFMGNERGH 603
 DB 361 GDKTIAFWLMDKMDYDFMALDPSPTPRIDRGIALHKTMLVMTGIGSGYLNFMGNERGH 420
 QY 604 PEWIDPBRGPOTLPYTKVLPQNNNSYDKCRRRFEDLGADFLRY 646
 DB 421 PEWIDPBRGPOTLPYTKVLPQNNNSYDKCRRRFEDLGADFLRY 463

RESULT 9

US-09-367-895-41
 / Sequence 41, Application US/09367895
 / Patent No. 6483009
 / GENERAL INFORMATION:
 / APPLICANT: POLISEN, PETER
 / TITLE OF INVENTION: ANTISENSE INTRON INHIBITION OF STARCH BRANCHING ENZYME
 / TITLE OF INVENTION: EXPRESSION
 / FILE REFERENCE: 078883/0112
 / CURRENT APPLICATION NUMBER: US/09/367,895
 / PRIOR FILING DATE: 1999-12-08
 / PRIOR APPLICATION NUMBER: PCT/IB98/00270
 / PRIOR FILING DATE: 1998-02-23
 / PRIOR APPLICATION NUMBER: GB/9703663.6
 / PRIOR FILING DATE: 1997-02-21
 / PRIOR APPLICATION NUMBER: GB/9706060.2
 / PRIOR FILING DATE: 1997-03-24
 / NUMBER OF SEQ ID NOS: 43
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 41
 / LENGTH: 906
 / TYPE: PRT
 / ORGANISM: Solanum tuberosum
 / US-09-367-895-41

Query Match 51.7%; Score 2156.5; DB 4; Length 906;
 Best Local Similarity 58.0%; Pred. No. 6.9e-196;
 Matches 400; Conservative 94; Mismatches 169; Indels 27; Gaps 7;

QY 90 IYEIDPTLKDFRSHLDYRYSEYRIRRAALDQHEGGLAEFSGYKLGFTSAGITYREW 149
 DB 99 LINDPTLEPYLDHRRHRKRKYVDQMLIEKYEGLPEEPAQGLKFGFNEDEDCIYREV 158
 QY 150 APGASALVDCPRNNWNPADTMTDIDYGVWEFLFNMDGSAIHSGRVYKRMTPSG 209
 DB 159 APAAGEAEVTDGFNGNGSNHMEKQDFGWSIRIP-DVDSKVIPIHNSVVKFRYHGG 217
 QY 210 V-KDSISAMIKFSVAPGEI--PFGIYVDPPEEKVYQHPQKPSHRIYESHIGMS 266
 DB 218 VAVDILPAWIKATADATFAAPYDGVYNDPPESEKHYHFPFRPRAPRIYEAHIGMS 277
 QY 267 SPEPKINSYANRDEVLPRIKLGYNVAVOIMAIQESYSYASFGYHVTNFPAPSSRGTPE 326
 DB 278 SSEPRVNSYREPADVDLPRIKANNYTVQIMAEHSYSGFGYHVTNFPAPSSRYGNPE 337
 QY 327 DIKSLIDRAHEGLLVNDIVHSHSNNTLDGNGPD---GTDTHYHGGGRHHMMWDS 363

DB 338 DLKYLIDKRAHSLGLOVLVDVHSHASNNTVDGNGPDIGGQSGQESYFHAGEBGYKLMDS 397
 QY 384 RLFNYSGVSWVTRFLISNARWMLLEEKFGFRDGYTSMMYTHHGLQMTFTGNYGEYGFPA 443
 DB 398 RLFNYSGVSWVTRFLISNARWMLLEEKFGFRDGYTSMMYTHHGLQMTFTGNYGEYGFPA 457
 QY 444 TVDVAVYLMVNDLHGLHPDASIGEDVSGMPTFCIPPDGSGVGFYRLHMAVADKMI 503
 DB 458 TVDVAVYLMVNDLHGLHPDASIGEDVSGMPTFCIPPDGSGVGFYRLHMAVADKMI 517
 QY 504 ELKQSDSWKMGDIVHTLTNRNMLEKCVTAESHDOALVGDKTIAFWLMDKMDYDFMA 562
 DB 518 DYIKKNDSDMSKETEYSSLTNRNRYEKCAVAFETHQOSLVGDKTIAFWLMDKMDYDFMA 577
 QY 563 LDRPSTPRIDRGIALHKTMLVMTGIGSGYLNFMGNERGHPEWIDPBRGPOTLPYTKV 622
 DB 578 CLTDAPVYDGRGIALHKTMLVMTGIGSGYLNFMGNERGHPEWIDPBRGPOTLPYTKV 626
 QY 623 PQNNNSYDKCRRRFEDLGADFLRYHGMQEBDOAMQHEEKYGPWTSHEYVSRKHEEDKY 682
 DB 627 EGNMNSYDKCRRRFEDLGADFLRYHGMQEBDOAMQHEEKYGPWTSHEYVSRKHEEDKY 686
 QY 683 IIPERGDVFPFPHNSNFPDYRGVSGRPDKYKVALDSDDALFGESRLDHDVYFTT- 741
 DB 687 VYPERGDLVFPFPHNSNFPDYRGVSGRPDKYKVALDSDDALFGESRLDHDVYFTT- 746
 QY 742 -----EHPHNDPFRSPSYTTPSRITAVY 764
 DB 747 EGIPGVETNFGRPNSFKVLSPARITCAV 776

RESULT 10

US-08-941-445A-17
 / Sequence 17, Application US/08941445A
 / Patent No. 6107060
 / GENERAL INFORMATION:
 / APPLICANT: Keeling, Peter
 / TITLE OF INVENTION: Starch Encapsulation
 / NUMBER OF SEQUENCES: 37
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 / STREET: 5370 Manhattan Circle
 / CITY: Boulder
 / STATE: CO
 / COUNTRY: US
 / ZIP: 80303
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/941,445A
 / FILING DATE: 30-SEP-1997
 / CLASSIFICATION: 800
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 60/026,855
 / FILING DATE: 30-SEP-1996
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Winner, Ellen P
 / REGISTRATION NUMBER: 28,547
 / REFERENCE/DOCKET NUMBER: 89-97
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (303) 499-8080
 / TELEFAX: (303) 499-8089
 / INFORMATION FOR SEQ ID NO: 17:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 822 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-941-445A-17

Tue Apr 20 10:02:28 2004

us-09-508-377-12.ra1

Page 7

Query Match 51.5%; Score 2146; DB 3; Length 822;
Best Local Similarity 57.0%; Pred. No. 5,8e-195;
Matches 395; Conservative 101; Mismatches 171; Indels 26; Gaps 6;

QY DGOKIYEIDPLTKDRSHLDYRSEYRIRAIRAIDQHEGGLAERSCYKLGFTSAEGIT 145
DB DHPITDIDPLTKDRSHLDYRSEYRIRAIRAIDQHEGGLAERSCYKLGFTSAEGIT 139
QY 146 YREWAPGAHSAALVGDENNPNADTMTRDDYGVWEIFLNNADSPALPHGSRVIRMD 205
DB 140 YREWAPGAHSAALVGDENNPNADTMTRDDYGVWEIFLNNADSPALPHGSRVIRMD 198
QY 206 TPGSVKDSISAMIKSVQAPGEI--PENGIIYDPEBEKRYVFOHPQKAPESLRITYESI 263
DB 199 HGVVWVDRIPALIRATYDASKFGADYDGVHMDPASERYTKHPRPSKPAAPRIYEAY 258
QY 264 GMSPEPKINSYANFRDEVLPRIKLGYNVQVQIMAIQESHYSYASFGYHTNFPAPSRFG 323
DB 259 GMSGKPAVSTYREFADNVLPRIRANNNTVOQMAVMEHSYASFGYHTNFPAPSRFG 318
QY 324 TPEDLKSIDRAHEGLLVMDIVSHSSNNTLDGLNGPD--GTDTHYHGGPRGHMM 380
DB 319 TPEDLKSIDRAHEGLLVMDIVSHSSNNTLDGLNGPD--GTDTHYHGGPRGHMM 378
QY 381 WDSRLFNYSWEVLRFLSNARWMLLEKYPDFRFGVTSNMYTHGLQMTFTGNGEYF 440
DB 379 WDSRLFNYSWEVLRFLSNARWMLLEKYPDFRFGVTSNMYTHGLQMTFTGNGEYF 438
QY 441 GPATVDAAVYVLMVNDLHGLHPDAVSGEDVSGMPTFCIPYDGGVGFDRYLMAVAD 500
DB 439 SLDTAVDAVYVLMVNDLHGLHPDAVSGEDVSGMPTFCIPYDGGVGFDRYLMAVAD 498
QY 501 KMIELKOSDES--WKGDIIVHTLTNRWMLLEKVTYAESHDQALVGDKTIAFWLMDKMYD 559
DB 499 RMIDYLNKDDSEWNGEIAHTLTNRWMLLEKVTYAESHDQALVGDKTIAFWLMDKMYD 558
QY 560 FMAIDRPSPTIRIDGIALHMKIRLVMTGLEGEGYINFMNGEFGHPMIDPRPQTLPTG 619
DB 559 GMSDLOPASPITDRIGALQMKIHFTMALQSDGYLNMGNBFGHPMIDPRPQTLPTG 610
QY 620 KVLPGNNNSYDKCRPRFDIGADPLRYHGMQEFDOAMQHLBEKYGEMTSEHOYSRKHEE 679
DB 611 ---EGNNWSYDKCRQMSLVDTDLRYKYMNAFDQAMNALDERFSFLSSKOIVSDNDE 667
QY 680 DKVITFERGDLVFNFNHNSNFPDVRVCGSRPGKRYKVALDSDDALFGGSRRLDHDVYF 739
DB 668 EKVIYFERGDLVFNFNHNSNFPDVRVCGSRPGKRYKVALDSDDALFGGSRRLDHDVYF 727
QY 740 TT-----EHPHNRPSFSVYTPSRVAVY 764
DB 728 TSPEGVPGVPEFTNPNRPNPSFKVLSPPRTCVAY 760

RESULT 11
US-09-731-166-14
Sequence 14, Application US/09731166
Patent No. 6639126
GENERAL INFORMATION:
APPLICANT: Sewall, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccharides
FILE REFERENCES: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
PRIOR APPLICATION NUMBER: 2000-12-06
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 822
TYPE: PRT
ORIGIN: Zeta Labs

US-09-731-166-14

Query Match 51.5%; Score 2146; DB 4; Length 822;
Best Local Similarity 57.0%; Pred. No. 5,8e-195;
Matches 395; Conservative 101; Mismatches 171; Indels 26; Gaps 6;

QY DGOKIYEIDPLTKDRSHLDYRSEYRIRAIRAIDQHEGGLAERSCYKLGFTSAEGIT 145
DB DHPITDIDPLTKDRSHLDYRSEYRIRAIRAIDQHEGGLAERSCYKLGFTSAEGIT 139
QY 146 YREWAPGAHSAALVGDENNPNADTMTRDDYGVWEIFLNNADSPALPHGSRVIRMD 205
DB 140 YREWAPGAHSAALVGDENNPNADTMTRDDYGVWEIFLNNADSPALPHGSRVIRMD 198
QY 206 TPGSVKDSISAMIKSVQAPGEI--PENGIIYDPEBEKRYVFOHPQKAPESLRITYESI 263
DB 199 HGVVWVDRIPALIRATYDASKFGADYDGVHMDPASERYTKHPRPSKPAAPRIYEAY 258
QY 264 GMSPEPKINSYANFRDEVLPRIKLGYNVQVQIMAIQESHYSYASFGYHTNFPAPSRFG 323
DB 259 GMSGKPAVSTYREFADNVLPRIRANNNTVOQMAVMEHSYASFGYHTNFPAPSRFG 318
QY 324 TPEDLKSIDRAHEGLLVMDIVSHSSNNTLDGLNGPD--GTDTHYHGGPRGHMM 380
DB 319 TPEDLKSIDRAHEGLLVMDIVSHSSNNTLDGLNGPD--GTDTHYHGGPRGHMM 378
QY 381 WDSRLFNYSWEVLRFLSNARWMLLEKYPDFRFGVTSNMYTHGLQMTFTGNGEYF 440
DB 379 WDSRLFNYSWEVLRFLSNARWMLLEKYPDFRFGVTSNMYTHGLQMTFTGNGEYF 438
QY 441 GPATVDAAVYVLMVNDLHGLHPDAVSGEDVSGMPTFCIPYDGGVGFDRYLMAVAD 500
DB 439 SLDTAVDAVYVLMVNDLHGLHPDAVSGEDVSGMPTFCIPYDGGVGFDRYLMAVAD 498
QY 501 KMIELKOSDES--WKGDIIVHTLTNRWMLLEKVTYAESHDQALVGDKTIAFWLMDKMYD 559
DB 499 RMIDYLNKDDSEWNGEIAHTLTNRWMLLEKVTYAESHDQALVGDKTIAFWLMDKMYD 558
QY 560 FMAIDRPSPTIRIDGIALHMKIRLVMTGLEGEGYINFMNGEFGHPMIDPRPQTLPTG 619
DB 559 GMSDLOPASPITDRIGALQMKIHFTMALQSDGYLNMGNBFGHPMIDPRPQTLPTG 610
QY 620 KVLPGNNNSYDKCRPRFDIGADPLRYHGMQEFDOAMQHLBEKYGEMTSEHOYSRKHEE 679
DB 611 ---EGNNWSYDKCRQMSLVDTDLRYKYMNAFDQAMNALDERFSFLSSKOIVSDNDE 667
QY 680 DKVITFERGDLVFNFNHNSNFPDVRVCGSRPGKRYKVALDSDDALFGGSRRLDHDVYF 739
DB 668 EKVIYFERGDLVFNFNHNSNFPDVRVCGSRPGKRYKVALDSDDALFGGSRRLDHDVYF 727
QY 740 TT-----EHPHNRPSFSVYTPSRVAVY 764
DB 728 TSPEGVPGVPEFTNPNRPNPSFKVLSPPRTCVAY 760

RESULT 12
US-08-104-158-2
Sequence 2, Application US/08104158
Patent No. 6215042
GENERAL INFORMATION:
APPLICANT: Wallmiller, Lothar
APPLICANT: Schmeiss, Uwe
APPLICANT: Kossmann, Jens
APPLICANT: Mueller-Roeber, Bernd
APPLICANT: Visser, Richard Gerardus Franciscus
TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gebt & Soffen


```

/ STREET: 1180 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-8403
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/104,158
/ FILING DATE: 13-AUG-1993
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP PCT/EP92/00302
/ FILING DATE: 11-FEB-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE P 41 04 782.6
/ FILING DATE: 13-FEB-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meilman, Edward A.
/ REGISTRATION NUMBER: 24,735
/ REFERENCE/DOCKET NUMBER: PA-1996 PCT (951-91)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-382-0700
/ TELEFAX: 212-382-0888
/ TELEX: 236925
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 566 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-104-158-2

Query Match      38.6%; Score 1608; DB 3; Length 566;
Best Local Similarity 57.8%; Pred. No. 5,1e-144;
Matches 298; Conservative 72; Mismatches 138; Indels 8; Gaps 5;

QY 90 IYEIDPTLKDPRSHLDYRSEYRIRAAIDQHEGGLAEFSRGYKLGFTSAEGITTYREW 149
DB 52 LNLNDPTLEPYLDHFRHMKRYVDQKMLIEKYEGPLEEPAQGYLKFGFNRDGCIVYREW 111
QY 150 APGAHSAALVGDENNPNADVTWTRDDYGVWEIFLPNNADGSPALPHGSRYKIRMDTPSG 209
DB 112 APAQAQAEVITGDNNGRYSNNHMEKQDFGWSIRIP-DVDSKPYIPHNRSKRFKFGNG 170
QY 210 V-KDSISAMIKFSVQAPGEI--PENGIIYDPPPEEKYVFOHPQKRPESLRITYESHIGNS 266
DB 171 VWVDRIPAWIKYATADATKFAAPYDGYWDPPESERYHFKPRPRAPRIYEAHVQMS 230
QY 267 SPEPKINSYANFRDEVLPRIKRLGYNAVQIMAIQESHVYASFGYHVTNFPADSSRFCTPE 326
DB 231 SSEPRVNSYREPADVLPRIKANNYTVQIMAIMESHVYSGFYHVTNFFAVSNRYGNPE 290
QY 327 DLKSLIDRAHEGLVMDIVYSHSSNNTLDGLNGD---GTDTHYFHGGRGHMMWMS 383
DB 291 DLKYLIDKAHSLGLQVLDVYVSHASNNVTDLGNGFDIGQGSQESYFFHAGERYHKLWDS 350
QY 444 TDVDAVYVYLMVNDLHGLHPDAVISIGEDVSGMFTFCIPVDDGGVGFYRLHMAVADKXI 503
DB 411 TDVDAVYVYLMANLNLHKLIFPDATVIAEDVSGMFGLSRPVSEGGIGFYRLAVALPDKXI 470
QY 384 RLFNYSWEVLRFLLSNARMWLEBYKDFGFRPDGVTSMMYTHGLQMTFTGYNGEYFGFA 443
DB 351 RLFNANWEVLRFLLSNARMWLEBYNDFGFRPDGITSMLYVHGIIMGFTGYNVEYFSEA 410
QY 444 TDVDAVYVYLMVNDLHGLHPDAVISIGEDVSGMFTFCIPVDDGGVGFYRLHMAVADKXI 503
DB 411 TDVDAVYVYLMANLNLHKLIFPDATVIAEDVSGMFGLSRPVSEGGIGFYRLAVALPDKXI 470
QY 504 ELKQ-SQDESQKMGDIYHTLTNRRLMEKCVTYAESHQDALVGDKTIAFWLMDKMYDQMA 562
DB 471 DYLKKNKDEDMKMEVSSLTNRRTYKCIYASHSDSIYGDKTIAFLNMKEMYSQMS 530
QY 471 DYLKKNKDEDMKMEVSSLTNRRTYKCIYASHSDSIYGDKTIAFLNMKEMYSQMS 530
DB 563 LDRPSTPRIDRGIALHKMIRLVTMGGEGEYLVNFMG 598
QY 563 LDRPSTPRIDRGIALHKMIRLVTMGGEGEYLVNFMG 598

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DB 531 CLTDASPVVDAGIALDKMIRHFFHNGLGRRGVPOFHG 566

RESULT 13
US-09-609-040-2
/ Sequence 2, Application US/09609040
/ Patent No. 6570066
/ GENERAL INFORMATION:
/ APPLICANT: Wilmittzer, et al.
/ TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE
/ FILE REFERENCE: 514413-3515.1
/ CURRENT APPLICATION NUMBER: US/09/609,040
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: PCT/EP92/00302
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 2
/ LENGTH: 566
/ TYPE: PRT
/ ORGANISM: Solanum tuberosum
/ US-09-609-040-2

Query Match      38.6%; Score 1608; DB 4; Length 566;
Best Local Similarity 57.8%; Pred. No. 5,1e-144;
Matches 298; Conservative 72; Mismatches 138; Indels 8; Gaps 5;

QY 90 IYEIDPTLKDPRSHLDYRSEYRIRAAIDQHEGGLAEFSRGYKLGFTSAEGITTYREW 149
DB 52 LNLNDPTLEPYLDHFRHMKRYVDQKMLIEKYEGPLEEPAQGYLKFGFNRDGCIVYREW 111
QY 150 APGAHSAALVGDENNPNADVTWTRDDYGVWEIFLPNNADGSPALPHGSRYKIRMDTPSG 209
DB 112 APAQAQAEVITGDNNGRYSNNHMEKQDFGWSIRIP-DVDSKPYIPHNRSKRFKFGNG 170
QY 210 V-KDSISAMIKFSVQAPGEI--PENGIIYDPPPEEKYVFOHPQKRPESLRITYESHIGNS 266
DB 171 VWVDRIPAWIKYATADATKFAAPYDGYWDPPESERYHFKPRPRAPRIYEAHVQMS 230
QY 267 SPEPKINSYANFRDEVLPRIKRLGYNAVQIMAIQESHVYASFGYHVTNFPADSSRFCTPE 326
DB 231 SSEPRVNSYREPADVLPRIKANNYTVQIMAIMESHVYSGFYHVTNFFAVSNRYGNPE 290
QY 327 DLKSLIDRAHEGLVMDIVYSHSSNNTLDGLNGD---GTDTHYFHGGRGHMMWMS 383
DB 291 DLKYLIDKAHSLGLQVLDVYVSHASNNVTDLGNGFDIGQGSQESYFFHAGERYHKLWDS 350
QY 444 TDVDAVYVYLMVNDLHGLHPDAVISIGEDVSGMFTFCIPVDDGGVGFYRLHMAVADKXI 503
DB 411 TDVDAVYVYLMANLNLHKLIFPDATVIAEDVSGMFGLSRPVSEGGIGFYRLAVALPDKXI 470
QY 504 ELKQ-SQDESQKMGDIYHTLTNRRLMEKCVTYAESHQDALVGDKTIAFWLMDKMYDQMA 562
DB 471 DYLKKNKDEDMKMEVSSLTNRRTYKCIYASHSDSIYGDKTIAFLNMKEMYSQMS 530
QY 563 LDRPSTPRIDRGIALHKMIRLVTMGGEGEYLVNFMG 598
DB 531 CLTDASPVVDAGIALDKMIRHFFHNGLGRRGVPOFHG 566

RESULT 14
US-09-579-365-2
/ Sequence 2, Application US/09579365
/ Patent No. 6566585
/ GENERAL INFORMATION:
/ APPLICANT: Martin QUENZ
/ TITLE OF INVENTION: GENETICALLY MODIFIED PLANT CELLS AND PLANTS WITH AN

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;; TITLE OF INVENTION: INCREASED ACTIVITY OF AN AMYLASE PROTEIN AND A
;; FILE OF INVENTION: BRANCHING ENZYME
;; FILE REFERENCE: 0147-0200P
;; CURRENT APPLICATION NUMBER: US/09/579,365
;; CURRENT FILING DATE: 2000-05-25
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 762
;; TYPE: PRT
;; ORGANISM: *Neisseria dentrificans*
US-09-579-365-2

Query Match 13.8%; Score 576; DB 4; Length 762;
Best Local Similarity 24.3%; Pred. No. 1,4e-45;
Matches 187; Conservative 126; Mismatches 227; Indels 210; Gaps 37;

QY 101 RSHLDYRGEYRIRRAIDQHEG---GLEAFSGYEKLG---FTR--SAGGTYREMAPGA 153
DB 106 REEDDYRFG---SALQHTDAMLGEGTHLRPEYTLGAHFAMDMGVSGVRFVAMPNA 159
QY 154 HSAALVGFENNNPNADTM--TRDDYGVWEIFLFPN-----NADGS---PAIPHG 197
DB 160 RAVSVIGENGMSRRHMRPHONGIMDIFIPGVGLNALYKFSVDANGIRKADPYA 219
QY 198 SRVXRMDTPSGVKDISAMIKFSVQAPGEIPENGIIYDPEPEEKYVFQHPQRPBSLR 257
DB 220 FGAELRPTASVYR-----GL---PAKAEAPFRRRANSVEAPIS 256
QY 258 IYESHIGMSPEEKIN---SYANPRDSEVLRIRKLGNAVOIMAIOHSYASFGYHTN 314
DB 257 IYEVHIGSVRRNENNYWLTYYTQADBLVYVXDMGTHIELPLSEPPGSGWGYQATG 316
QY 315 FAPSSRFGTPEDLKSLIDRAHELGILVMDIVHSHSSNNTLDGLNGFDGDTYFPGP 374
DB 317 LVAFTRFSGPDLKALIDAAHAAIGSVILDDVAGHPTDD--HGLNTPDGI--ALYEHADP 374
QY 375 R-GHHMMDSRLFNYSWEVLARLLSNARWLEBYKDFGDFGVTSMMYTHGLQMTFT 433
DB 375 RGGYHODMNTLLIYNFGSEVKNFLQGNALYIERFEGDGRVDAVSMIYRN-----YS 428
QY 434 GNYGEY---FGATVDVAIVYLMVNDLHGLHDAVSGEDVSGMPTFCIPYPDGVG 489
DB 429 RKDGEWIPRKYGSSENLIAFLRQTNVAVLKSETPGGSFAEST---SFADVTREAGLN 485
QY 490 FYRLIMAVADKKI--ELIKQSDSWKMGDIVHTLTNRMLEKCVT-----YAE----- 536
DB 486 FDFKXMMG---WMNDTLRYMGE---DGVH---RKYHNGKMTFGMMYGYSENFLVPL 532
QY 537 SHDQALVGDXTIA-----FWLMDKDM---YDFMALDRPSTPRIDGIALHKMLRLVTMG 587
DB 533 SHDEVVHGKSLILGKMPGDMQGFANLRAVYGFV-----YG 568
QY 588 LGGEGVLNMGNEFGH--PEWIDFPRGPQTLPTGKVLFGNNNSYDKCRRFLGADFLRY 646
DB 569 FPGKLL--FMGNEFAQREM--NYOEG-----LDW 595
QY 647 H-----GMQEPDQAMQHL-----EKKYGFMTSEHQYVSRGHEEDKYLIF 685
DB 596 HLLDEAGMHKGYQDYVRLNHTYTAAPLYQDQGEF-----EWLVADDSNSVFFV 650
QY 686 EREGD---LVFVFN-----HMSNSFDPYRVGCSRPKGYKVALDSDDALFGFSRLDH 734
DB 651 ERDRAGNIIIVSNFTPVREH-----YRFGVNAAPGRYTEILNSDRTOYGQ--SGIAN 702
QY 735 DVDFYFTEHHDNRPRSFSVYTPSRATVY 764
DB 703 GADITAEVPSHGKQSLSLTLP--LATVY 731

;; Patent No. 6608018
;; GENERAL INFORMATION:
;; APPLICANT: No. 6608018ozymes A/S
;; APPLICANT: Shinohara, Mari U.
;; TITLE OF INVENTION: Polypeptides having branching enzyme activity and nucleic acids
;; FILE REFERENCE: 5860.200-US
;; CURRENT APPLICATION NUMBER: US/09/537,120
;; CURRENT FILING DATE: 2001-08-17
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: Patent In version 3.1
;; SEQ ID NO 2
;; LENGTH: 621
;; TYPE: PRT
;; ORGANISM: *Rhodothermus obamensis*
US-09-537-120-2

Query Match 13.0%; Score 541.5; DB 4; Length 621;
Best Local Similarity 26.2%; Pred. No. 2e-42;
Matches 175; Conservative 114; Mismatches 243; Indels 135; Gaps 28;

QY 118 IDHEGGLAERSGYEKLGFTSASGITYREMAPGAHSALVGFENNNPNADTMTRDDY 177
DB 9 IRRWESG--TFYDSYRKLGANHDDEGTWFCWAPHADGVSVLGAFDMNPENAPLEHYGG 66
QY 178 GVWEIFLNNADGSAIPHGRVKIRMDTPSGVKDISAMIKFSVQAPGEIPENGIT 233
DB 67 GLMAGYVPGAREG---HTYKXIRIRHGFYQADKTPYA---FAMEPPTGSPTEGLASII 118
QY 224 -----YDPEPEEKYVFGHPQ--KRPESLRITYESHIG---SSPEKINSYANFRDEVL 283
DB 119 TRLDYTHMD---DEMMRRKRPASLYEPVSTIYVHLSGWRHRRKPGESF--SYRELAPLA 173
QY 284 PRKLGNAVOIMAIOHSYASFGYHTNFPAPSSRFGTPEDLKSLIDRAHELGILV 343
DB 174 DYQMGSGTHBELLVMEHPYTGSGWGYVGYAPFRFGSPDDMLYLDYHQRGIGVI 233
QY 344 MDIVHSSNNTLDGLNGFDGDTYFHGGRGHHMMDSRLFNYSWEVLARLLSNARW 403
DB 224 LDWVSHPAADP--QGLVFEFDGTTLPEDYDPRKRYHHPDMGTYVVDYKPKGVRLISNALF 292
QY 404 WLEEKYKPGFRPDGVTSMYTHHGLQMTFTGNYGEYFGATVDVAIVYLMVNDLHGLH 463
DB 293 WLEKTHVGLRVDVAWSMLYRYS--RKEWTPN--TFGRENLEALDIFIKKEETVYLHP 348
QY 464 PDAVSGEDVSGMPTFCIPVDPGVGFYRLHMAVADKKIELIKQSDSWKMGDIVHTLT 523
DB 349 PEAMTIAESTAMPVSAPATYNNAGLFLYK-----WNNGMNHTLD 389
QY 524 NRMWLEKCVTAESHDQALVGDXTIAFWLMDKDMYDFMALDRPSTPRIDGIALHKM 580
DB 390 ---YIQRDPIYKXAHDEL---TSLMYAFSEHY--VLPLSHDEVH--GKGSJMGKMPGD 440
QY 581 -----IRLVTMGIGGE--GYLNFMGNEFG--HPEWIDFPRGPQTLPTGKVLFGNNNSYD 630
DB 441 DMQKAAIRLLRFGHMGHPGKLLFMGSGFGQHHE-----NHTT-- 480
QY 631 KCRRRFDLGDADFLRYHGMQEPDQAMQHL-----EKKYGFMTSEHQYVSRGHEEDK 681
DB 481 ---QLEMHLLDQPY--HRIQLMVCOLNHYKRNPAALMHGGRBEF-----EMIDFSRBDQS 531
QY 682 VIFERGD---LVFVFN-----HMSNSFDPYRVGCSRPKGYKVALDSDDALFGFSRLDH 728
DB 532 VICYRKXAGRWLLFLVNFPTPVREH-----YRVGVPIGFGWHEVLNSDAVAYGSGSM 584
QY 729 --FSRLD 733
DB 585 GNFGRAVE 591

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 08:38:16 ; Search time 48 Seconds
(without alignments)
4410.770 Million cell updates/sec

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Perfect score: 4169
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1124875 segs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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18:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3588.5	86.1	814	14	US-10-171-008-10
2	3363	80.7	855	9	US-09-792-127-4
3	3348.5	80.3	829	9	US-09-792-127-5
4	3342.5	80.2	798	12	US-10-336-753-70
5	3342.5	80.2	870	12	US-10-336-753-54
6	3329	79.9	695	9	US-09-792-127-2
7	3325.5	79.8	870	12	US-10-424-599-273691
8	3175	75.2	878	14	US-10-254-534-2
9	3135	75.2	882	14	US-10-056-454-15
10	2213	53.1	464	14	US-10-254-534-4
11	2146	51.5	776	12	US-10-336-753-56
12	2146	51.5	822	14	US-10-171-008-9
13	1978	47.0	674	12	US-10-425-114-53683
14	1917.5	46.0	874	15	US-10-369-493-3969
15	1915	45.9	421	12	US-10-425-114-45676

16	1896	45.5	681	15	US-10-369-493-5706	Sequence 5706, Ap
17	1795.5	43.1	704	15	US-10-369-493-11720	Sequence 1720, Ap
18	1656	39.7	647	15	US-10-369-493-10283	Sequence 10283, A
19	1642	39.4	546	14	US-10-171-008-8	Sequence 8, Appl1
20	1284	30.8	309	14	US-10-171-008-4	Sequence 4, Appl1
21	851	20.4	337	12	US-10-262-511-108	Sequence 108, App
22	745.5	17.9	375	12	US-10-424-599-283934	Sequence 283934, A
23	579	13.9	726	15	US-10-369-493-198590	Sequence 198590, A
24	575.5	13.8	750	15	US-10-369-493-19848	Sequence 19848, A
25	574	13.8	737	15	US-10-369-493-12299	Sequence 12299, A
26	573	13.5	710	15	US-10-369-493-12299	Sequence 2780, Ap
27	564.5	13.5	731	9	US-09-738-626-4854	Sequence 4854, Ap
28	560.5	13.4	159	12	US-10-369-493-20849	Sequence 20849, A
29	559	13.4	159	12	US-10-424-599-230110	Sequence 230110, A
30	558	13.4	730	12	US-10-282-122A-58499	Sequence 58499, A
31	556.5	13.3	736	15	US-10-369-493-20951	Sequence 20951, A
32	554	13.3	755	15	US-10-369-493-20951	Sequence 19307, A
33	553.5	13.3	728	15	US-10-369-493-19307	Sequence 23588, A
34	553.5	13.3	785	12	US-10-336-753-36	Sequence 36, Appl
35	553	13.3	617	15	US-10-369-493-9891	Sequence 9891, Ap
36	550.5	13.2	705	15	US-10-369-493-632	Sequence 632, App
37	549.5	13.2	630	15	US-10-369-493-50	Sequence 50, Appl
38	543	12.9	719	15	US-10-369-493-10019	Sequence 10019, A
39	537	12.9	732	12	US-10-389-647-471	Sequence 471, App
40	532	12.8	628	15	US-10-369-493-9028	Sequence 9028, Ap
41	532	12.8	677	12	US-10-200-055-63	Sequence 63, Appl
42	526	12.6	717	15	US-10-369-493-7769	Sequence 7769, Ap
43	520.5	12.5	718	15	US-10-369-493-15576	Sequence 15576, A
44	520.5	12.5	718	15	US-10-369-493-15952	Sequence 15952, A
45	520.5	12.5	720	15	US-10-369-493-16316	Sequence 16316, A

ALIGNMENTS

RESULT 1	US-10-171-008-10
Sequence 10, Appl1	US/10171008
Publication No. US2003012653A1	
GENERAL INFORMATION:	
APPLICANT: Ursula Uwer	
APPLICANT: Claus Froberg	
APPLICANT: Jens Pilling	
APPLICANT: Volker Landshutze	
TITLE OF INVENTION: Transgenic plants synthesising high amylose starch	
FILE REFERENCE: VOS-36	
CURRENT APPLICATION NUMBER: US/10/171,008	
CURRENT FILING DATE: 2002-09-13	
PRIOR APPLICATION NUMBER: DE 10 12 8363.6	
PRIOR FILING DATE: 2001-06-12	
NUMBER OF SEQ ID NOS: 10	
SOFTWARE: Patentln version 3.1	
SEQ ID NO 10	
LENGTH: 814	
TYPE: PRT	
ORGANISM: Zea mays	
US-10-171-008-10	
Query Match	86.1%; Score 3588.5; DB 14; Length 814;
Best Local Similarity	84.7%; Pred. No. 0;
Matches 663; Conservative 32; Mismatches 49; Indels 39; Gaps 4;	
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38 LSSAEVVDVQPELOPE-----AEI-----TVK-TSSSPQTTSVAVAAGSVAE	85
56 -----GIVETITGVTKGVVELVGEKPRVVPKPDQOKIYEIDPTLKDFFRSH	103
86 ERPELEEVIGVGTGKIKIGAGIKAKAPLVEKPRVIPPQDQORITIDPMKEGFRCH	145
104 LDVRYEYRRIRAIQHEGGLAFAFSRGYELGFTRSAGITTYEMAFGAHSAALVGFN	163
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QY 164 NNNPNADTMRDDYGMWELFLPNNADGSPAI PHGSRVKIRMDTPSGYKDSISAMIKESVQ 223
DB 206 NNNPNADMARBNYGMWELFLPNNADGSPAI PHGSRVKIRMDTPSGYKDSIPAMIKESVQ 265
QY 224 ARGEIPFNQIYDPPPEEKYVFOHPQRPBESLRITYSHIGMSPEPKINSYANFRDEVL 283
DB 266 ARGEIPFNQIYDPPPEEKYVFOHPQRPBESLRITYSHIGMSPEPKINSYANFRDEVL 325
QY 284 PRKRGYNVAVOVMAIOEHSYVAFGYHVNFFAPSSRFGTPEDLKSLIDRAHEGLLV 343
DB 326 PRKRGYNVAVOVMAIOEHSYVAFGYHVNFFAPSSRFGTPEDLKSLIDRAHEGLLV 385
QY 344 MDIVSHSSNNITDGLNGFDGTDHYFHGGRGHMMWDSRLFNYSWELRFLLSNARW 403
DB 386 MDIVSHSSNNITDGLNGFDGTDHYFHGGRGHMMWDSRLFNYSWELRFLLSNARW 445
QY 404 WLEBYKDFRFDGVTSMYTHHGLQVTFGNYSYFGFATDVAVYLMVNDLIRGLY 505
DB 446 WLEBYKDFRFDGVTSMYTHHGLQVTFGNYSYFGFATDVAVYLMVNDLIRGLY 505
QY 464 PDVASTIGEDVSGMPTFCIPVDGSGVDFYRLHMAVADKWIILKQSDSWKMGDI VHTLT 523
DB 506 PDVASTIGEDVSGMPTFCIPVDGSGVDFYRLHMAVADKWIILKQSDSWKMGDI VHTLT 565
QY 524 NRMWLEKCVTYAESHDQALVGDKTIAFWLMDKMYDFMALDRPSTPRIDRGIALHKMIRL 583
DB 566 NRMWLEKCVTYAESHDQALVGDKTIAFWLMDKMYDFMALDRPSTPRIDRGIALHKMIRL 625
QY 584 VTMGLGEGYLINFNGNEBPEWIDPRGPGDTLPFGKYLPGNNNSYDKCRRRFDGADDF 643
DB 626 VTMGLGEGYLINFNGNEBPEWIDPRGPGDTLPFGKYLPGNNNSYDKCRRRFDGADDF 685
QY 644 LRHGMQEFQOAMHLEEKYFMTSEHQYSRKHEEDKVIIFERGDIVFVNFHMSNFF 703
DB 686 LRHGMQEFQOAMHLEEKYFMTSEHQYSRKHEEDKVIIFERGDIVFVNFHMSNFF 745
QY 704 DYRVGCSRPGKYKVALDSDDALFGGFSRLDHDVDVFTTEHPHNDPRSFSYVTPSRITAV 763
DB 746 DYRVGCSRPGKYKVALDSDDALFGGFSRLDHDVDVFTTEHPHNDPRSFSYVTPSRITAV 805
QY 764 YA 765
DB 806 YA 807

```

RESULT 2

```

US-09-792-127-4
; Sequence 4, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlsstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIB
; FILE REFERENCE: B81439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-792-127-4

```

Query Match 80.7%; Score 363; DB 9; Length 855;
 Best Local Similarity 79.5%; Pred. No. 1,3e-306;
 Matches 607; Conservative 75; Mismatches 68; Indels 14; Gaps 4;

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QY 7 SGATIGVARRPAAOP-----BELOIPEDIEAQTAENVMTGTGAETLESSEPTQIVETI 61
DB 98 SGGT-----PESIDPVPVFDSDDLKVP-FIDET---SLQDGGEDSIWSETNQVSEID 148
QY 62 TDGVTKGVKELVYVSEKPRVPRKPGDGOKIYEIDPTLKDRSHLDYVSEYRRIRAAIDQH 121
DB 149 AEDTSRMKESSTREKRLILPPPGNGQCIYEIDPTLRDKYHLEYVSLYRRIRSDIDEH 208
QY 122 EGGLEAFSRGYEKLGFTEGAGIITYREMAFGAHSAAVQDFFNNMNNADTMRDDYGMW 181
DB 209 ECGMDVFSRGYKFKPFMSASAGITYREMAFGAHSAAVQDFFNNMNNADTMRDDYGMW 268
QY 182 IFLPNNADGSPAI PHGSRVKIRMDTPSGYKDSISAMIKESVQARGEIPFNQIYDPEEE 241
DB 269 IFLPNNADGSPAI PHGSRVKIRMDTPSGYKDSISAMIKESVQARGEIPFNQIYDPEEE 328
QY 242 KYVFOHPQRPBESLRITYSHIGMSPEPKINSYANFRDEVLPRIRLGYNAVQVMAIOE 301
DB 329 KYVFOHPQRPBESLRITYSHIGMSPEPKINSYANFRDEVLPRIRLGYNAVQVMAIOE 388
QY 302 HSYVAFGYHVNFFAPSSRFGTPEDLKSLIDRAHEGLLVMDIYHSSNNITDGLNG 361
DB 369 HSYVAFGYHVNFFAPSSRFGTPEDLKSLIDRAHEGLLVMDIYHSSNNITDGLNG 448
QY 362 PDGTDHYFHGGRGHMMWDSRLFNYSWELRFLLSNARWLEEKYKDFRFDGVTSM 421
DB 449 PDGTDHYFHGGRGHMMWDSRLFNYSWELRFLLSNARWLEEKYKDFRFDGVTSM 508
QY 422 MYTHHGLQVTFGNYSYFGFATDVAVYLMVNDLIRGLHAPDAVSIGEDVSGMPTFCI 481
DB 509 MYTHHGLQVTFGNYSYFGFATDVAVYLMVNDLIRGLHAPDAVSIGEDVSGMPTFCI 568
QY 482 PYVDGSGVDFYRLHMAVADKWIILKQSDSWKMGDI VHTLTNRNMLEKCVTYAESHDQ 541
DB 569 PYVDGSGVDFYRLHMAVADKWIILKQSDSWKMGDI VHTLTNRNMLEKCVTYAESHDQ 628
QY 542 LVGDKTIAFWLMDKMYDFMALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLINFNGNEF 601
DB 629 LVGDKTIAFWLMDKMYDFMALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLINFNGNEF 688
QY 602 GHPEWIDPRGPGDTLPFGKYLPGNNNSYDKCRRRFDGADDFLRHGMQEFQOAMHLE 661
DB 689 GHPEWIDPRGPGDTLPFGKYLPGNNNSYDKCRRRFDGADDFLRHGMQEFQOAMHLE 748
QY 662 KYGFMTEHQYVSRKHEEDKVIIFERGDIVFVNFHMSNFFDYRVGCSRPGKYKVALDS 721
DB 749 KYGFMTEHQYVSRKHEEDKVIIFERGDIVFVNFHMSNFFDYRVGCSRPGKYKVALDS 808
QY 722 DDALFGGFSRLDHDVDVFTTEHPHNDPRSFSYVTPSRITAVYA 765
DB 809 DDALFGGFSRLDHDVDVFTTEHPHNDPRSFSYVTPSRITAVYA 852

```

RESULT 3

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US-09-792-127-5
; Sequence 5, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlsstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIB
; FILE REFERENCE: B81439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 829
; TYPE: PRT

```

Tue Apr 20 10:02:28 2004

us-09-508-377-12.rapb

Page 3

ORGANISM: Hordeum vulgare
US-09-792-127-5

Query Match 80.3%; Score 3348.5; DB 9; Length 829;
Best Local Similarity 79.1%; Pred. No. 2.8e-305;
Matches 605; Conservative 72; Mismatches 75; Indels 13; Gaps 3;

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QY      8 GATLVAREPAAA-----OPEELQIP--EDIEBQTAENVNTGTAEKLESSEPTQIVET 60
DB      68 GSGSGSGTSPISIGSVQFESDDLEVPRIID-----EPLSHDGEDTIRSEETQVTEBI 121
QY      61 ITDGVTKYKVELVGEKPRVVPKPGDQKTYEIDPTLKDRSHLDYRYSEYRRIRRAIDQ 120
DB      122 DAGVSRMKESTVKKIRIVPQPGNGQQIYDIDPMLRDKYHLEYRSLYRRIRRSIDE 181
QY      121 HEGGLEAFSGYKELGFTRSAEGITYREMAPGAHSALVGFNNMNPADTMTEDDYGVW 180
DB      182 YDGMGMVFSKGYEKFGFVRSABEGITYREMAPGAHSALVGFNNMNPADTMTEDDYGVW 241
QY      181 ELFLPNNADGSPAIPIHSGRYKIRMDTPSGVDSISAMIKESVQAPGEIPENGIIYDPEE 240
DB      242 ELFLPNNADGSPAIPIHSGRYKIRMDTPSGVDSISAMIKESVQAPGEIPENGIIYDPEE 301
QY      241 EKYVFOHPQKRPESLRIYSHIGMSPEPKINSYANFRDEVLPRIKRLGYNVQVMAIQ 300
DB      302 EKYVFKHPQKRPESLRIYSHIGMSPEPKINSYANFRDEVLPRIKRLGYNVQVMAIQ 361
QY      301 EHSYVASFQYHVNFPAPSRFGTPEDLKSLIDRAHELGILVMDIVSHSSNNTLDGLN 360
DB      362 EHSYVASFQYHVNFPAPSRFGTPEDLKSLIDRAHELGILVMDIVSHSSNNTLDGLN 421
QY      361 GPDGIDTHYFHGGPRGHMMWDSRLFNYSGWELRFLLSNARWLLEBKYPDFRPGVTS 420
DB      422 GPDGIDTHYFHGGPRGHMMWDSRLFNYSGWELRFLLSNARWLLEBKYPDFRPGVTS 481
QY      421 KMYTHHGLQMTFTNGYNGEYGFATDVAVYTLMLVNDLHGLHPDAYSIGDVSMPFFC 480
DB      482 KMYTHHGLQMTFTNGYNGEYGFATDVAVYTLMLVNDLHGLHPDAYSIGDVSMPFFC 541
QY      481 IPRPDGCVGDYLLHMAVADKWTIELLKQSDSEWKGQDVHTLTNRMLLEKVTYAESHDQ 540
DB      542 LPVQGVGVGDYLLHMAVADKWTIELLKQSDSEWKGQDVHTLTNRMLLEKVTYAESHDQ 601
QY      541 ALVGDXTIAFWLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVYTMGLGEGYINPMNE 600
DB      602 ALVGDXTIAFWLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVYTMGLGEGYINPMNE 661
QY      601 FGHPEWIDFPRGQPTLTPTGYLVLPNNNSYDKCRRRFDLGDADFLRYHMOEFDQMOHLE 660
DB      662 FGHPEWIDFPRGQPTLTPTGYLVLPNNNSYDKCRRRFDLGDADFLRYHMOEFDQMOHLE 721
QY      661 EKXGEMSEHOYRKKEBEDKVIIFERGDVLFVFNHNSNFFDYRVCGRPGKTKVALD 720
DB      722 EKXGEMSDHOYRKKEBEDKVIIFERGDVLFVFNHNSNFFDYRVCGRPGKTKVALD 781
QY      721 SDDALFGGFSRLDHDVDVFTTEHHPDNRPRSFSYVTPSRITAVVYA 765
DB      782 SDDALFGGFSRLDHDVDVFTTEHHPDNRPRSFSYVTPSRITAVVYA 826
```

RESULT 4
US-10-336-753-70
; Sequence 70; Application US/10336753
; Publication No. US20030226176A1

GENERAL INFORMATION:
APPLICANT: Guan, Hanping
APPLICANT: Keeling, Peter L.
TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
FILE REFERENCE: 2461-52
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US/09/402.254

PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,935
PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 70
LENGTH: 798
TYPE: PRT
ORGANISM: Zea mays
US-10-336-753-70

Query Match 80.2%; Score 3342.5; DB 12; Length 798;
Best Local Similarity 76.0%; Pred. No. 3.8e-305;
Matches 613; Conservative 65; Mismatches 76; Indels 53; Gaps 5;

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QY      4 FAVSGATIGVA-RPP-----AAAQPEELQI 27
DB      3 FRVSAVLGCAVRAARLITGGGEGSLVFRITGLEFLITGAVGCGSTGAMAAAAARAAV 62
QY      28 PEDIEBQTAENVNTGTAEKLESSE-----PTQIVETITDGVTKYKVELVGEKPRV 81
DB      63 PEGEND-----GLASRADSAQFQSDLEVPDISERTTGA--GVADAQALNRVRVV 111
QY      82 PEPGCGQKTYEIDPTLKDRSHLDYRYSEYRRIRRAIDHGGGLEAFSGRYKELGFTRSA 141
DB      112 PEPGCGQKTYEIDPTLKDRSHLDYRYSEYRRIRRAIDHGGGLEAFSGRYKELGFTRSA 171
QY      142 EBITREMAPGAHSALVGFNNMNPADTMTEDDYGVWEIFLPPNADGSPAIPIHSGRYK 201
DB      172 EBITREMAPGAHSALVGFNNMNPADTMTEDDYGVWEIFLPPNADGSPAIPIHSGRYK 231
QY      202 IRMDTPSGVDSISAMIKESVQAPGEIPENGIIYDPEEZYKYPQHPQKRPESLRIYES 261
DB      223 YAMDTPSGVDSISAMIKESVQAPGEIPENGIIYDPEEZYKYPQHPQKRPESLRIYES 291
QY      262 HIGMSPEPKINSYANFRDEVLPRIKRLGYNVQVMAIQSHSYASFQYHVNFPAPSR 321
DB      292 HIGMSPEPKINSYANFRDEVLPRIKRLGYNVQVMAIQSHSYASFQYHVNFPAPSR 351
QY      322 FGTPEDLKSLIDRAHELGILVMDIVSHSSNNTLDGLNFPDGDTHYFHSRGRGHMMW 381
DB      352 FGTPEDLKSLIDRAHELGILVMDIVSHSSNNTLDGLNFPDGDTHYFHSRGRGHMMW 411
QY      382 DSRLEFNYSWEVLRLLSNARWLLEBKYPDFRPGVTSKMYTHHGLQMTFTNGYNGEY 441
DB      412 DSRLEFNYSWEVLRLLSNARWLLEBKYPDFRPGVTSKMYTHHGLQMTFTNGYNGEY 471
QY      442 FATDVAVYTLMLVNDLHGLHPDAYSIGDVSMPFFCPLVPDGGVGFDRYLLHMAVADK 501
DB      472 FATDVAVYTLMLVNDLHGLHPDAYSIGDVSMPFFCPLVPDGGVGFDRYLLHMAVADK 531
QY      502 WIELKQSDSEWKGQDVHTLTNRMLLEKVTYAESHDQALVGBKTIAPFWLMDKMDYDFM 561
DB      532 WIELKQSDSEWKGQDVHTLTNRMLLEKVTYAESHDQALVGBKTIAPFWLMDKMDYDFM 591
QY      562 ALDRPSTPRIDRGIALHKMIRLVYTMGLGEGYINPMNEFGHPWIDPFRGQPTLTPTGY 621
DB      592 ALDRPSTPRIDRGIALHKMIRLVYTMGLGEGYINPMNEFGHPWIDPFRGQPTLTPTGY 651
QY      622 LPNNNSYDKCRRRFDLGDADFLRYHMOEFDQMOHLEBKYTEMTSDHOYIYRKKEBEDK 681
DB      652 LPNNNSYDKCRRRFDLGDADFLRYHMOEFDQMOHLEBKYTEMTSDHOYIYRKKEBEDK 711
QY      682 VIFFERGDVLFVFNHNSNFFDYRVCGRPGKTKVALDSDDALFGGFSRLDHDVDVFTT 741
DB      712 VIFFERGDVLFVFNHNSNFFDYRVCGRPGKTKVALDSDDALFGGFSRLDHDVDVFTT 771
QY      742 EHPDNRPRSFSYVTPSRITAVVYALTE 768
DB      772 DCSHDNRPRSFSYVTPSRITAVVYALTE 798
```

RESULT 5

US-10-336-753-54
 / Sequence 54, Application US/10336753
 / Publication No. US20030226176A1
 / GENERAL INFORMATION:
 / APPLICANT: Guan, Hanning
 / APPLICANT: Keeling, Peter L.
 / TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
 / TITLE OF INVENTION: HOSTS
 / FILE REFERENCE: 2461-52
 / CURRENT APPLICATION NUMBER: US/10/336,753
 / CURRENT FILING DATE: 2003-01-06
 / PRIOR APPLICATION NUMBER: US/09/402,254
 / PRIOR FILING DATE: 1999-10-01
 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
 / PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
 / PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
 / NUMBER OF SEQ ID NOS: 77
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 54
 / LENGTH: 870
 / TYPE: PRT
 / ORGANISM: Zea mays
 / US-10-336-753-54

Query Match 80.2%; Score 3342.5; DB 12; Length 870;
 Best Local Similarity 76.0%; Pred. No. 1.1e-304;

Matches 613; Conservative 65; Mismatches 76; Indels 53; Gaps 5;

4 PAVSAGATGVA-RPP-----AAQPELQI 27
 3 FRVSGAVVGVAVRPRLTGGGSGSLVFRHTGLFTRGARVCGSTTGAMRAAAAKAV 62
 28 PEDIEQTAAYVMGTGTAKEKLESE-----PTGIVETITDGTGKVELVGEKPRV 81
 63 PEGEND-----GLASRADSAQFQSDLEVPDISEETCGA--GVADAQALNVRV 111
 82 PKPGDQKIYEIDPFLKDFRSHLDVRYSEYRIRAIADHDEGLEAFSGYEGLGFTRSA 141
 112 PPSDQKIFQIDPMLQGYKHLERYSLYRIRISDIDHEGGLXPSSEYKFGFNASH 171
 142 EGITREAVAPGASHAALVGDFFNNMNPADTMRDYGWVEIFLNNADSPALPHSGRYK 201
 172 EGITREAVAPGASHAALVGDFFNNMNPADTMRDYGWVEIFLNNADSPALPHSGRYK 221
 202 IRMDTPSGVKDSISAMIKFSVQAPGEIPNGIYYDPPEEEKYVFGHPQKRPESLR 261
 232 VRMDTPSGVKDSISAMIKFSVQAPGEIPNGIYYDPPEEEKYVFGHPQKRPESLR 291
 262 HITGMSPPPKINSYANFRDEVLPRIKLGYNVAVQMAIOEHSYVSGFYHVTNFPAPSSR 321
 292 HVGMSPPPKINTYVNFDEVLPRIKLGYNVAVQMAIOEHSYVSGFYHVTNFPAPSSR 351
 322 FGTPEDLKSLIDRAHELGILVLMIDIVHSHSNNTLDGLNGFGDGTDTHTYFHGGRHMM 381
 352 FGTPEDLKSLIDRAHELGILVLMIDIVHSHSNNTLDGLNGFGDGTDTHTYFHGGRHMM 411
 382 DSRLFNYSWEVLRLFLSNARWMLBEYKFDGFRPDGVTSMYTHGLOVFTNFEYFG 441
 412 DSRLFNYSWEVLRLFLSNARWMLBEYKFDGFRPDGVTSMYTHGLOVFTNFEYFG 471
 442 PATDVAVYVYLMVNDLHGLHPDVAISIGEDVSGMPTFCIPVDDGAVGDFYRLHMAVADK 501
 472 PATDVAVYVYLMVNDLHGLHPDVAISIGEDVSGMPTFCIPVDDGAVGDFYRLHMAVADK 531
 502 WIELLKQSDSEWKGADIVHTLTNRRLWLEKCVTYAESHDQALVGDKTIAPFLMDKMDYDFM 561
 532 WIELLKQSDSEWKGADIVHTLTNRRLWLEKCVTYAESHDQALVGDKTIAPFLMDKMDYDFM 591
 562 ALDRSTPRIDRGIALHKKIRLTVTNGIGSGGYLNFPMNGNEFGEHWIDFPFGQTLPIPGKV 621

RESULT 6

US-09-792-127-2
 / Sequence 2, Application US/09792127
 / Patent No. US2002002713A1
 / GENERAL INFORMATION:
 / APPLICANT: Allen, Steve
 / APPLICANT: Beckles, Diane M.
 / APPLICANT: Butler, Karla
 / APPLICANT: Pearlstein, Rich
 / TITLE OF INVENTION: Starch Branching Enzyme IIB
 / FILE REFERENCE: BB1439 US NA
 / CURRENT APPLICATION NUMBER: US/09/792,127
 / CURRENT FILING DATE: 2001-02-23
 / PRIOR APPLICATION NUMBER: 60/186098
 / PRIOR FILING DATE: 2000-03-01
 / NUMBER OF SEQ ID NOS: 5
 / SOFTWARE: Microsoft Office 97
 / SEQ ID NO 2
 / LENGTH: 695
 / TYPE: PRT
 / ORGANISM: Triticum aestivum
 / US-09-792-127-2

Query Match 79.9%; Score 3329; DB 9; Length 695;
 Best Local Similarity 85.4%; Pred. No. 1.5e-303;

Matches 589; Conservative 60; Mismatches 41; Indels 0; Gaps 0;

76 EKRRVVPKPGDQKIYEIDPFLKDFRSHLDVRYSEYRIRAIADHDEGLEAFSGYEGL 135
 3 EKRIILPPNGQKIYEIDPFLKDFRSHLDVRYSEYRIRAIADHDEGLEAFSGYEGL 62
 136 GFTRSAEGITYREAVAPGASHAALVGDFFNNMNPADTMRDYGWVEIFLNNADSPALP 195
 63 GFTRSAEGITYREAVAPGASHAALVGDFFNNMNPADTMRDYGWVEIFLNNADSPALP 122
 196 HGSRRVKTMDTPSGVKDSISAMIKFSVQAPGEIPNGIYYDPPEEEKYVFGHPQKRPES 255
 123 HGSRRVKTMDTPSGVKDSISAMIKFSVQAPGEIPNGIYYDPPEEEKYVFGHPQKRPES 182
 256 LRIYESTITGMSPPPKINSYANFRDEVLPRIKLGYNVAVQMAIOEHSYVSGFYHVTN 315
 183 LRIYESTITGMSPPPKINSYANFRDEVLPRIKLGYNVAVQMAIOEHSYVSGFYHVTN 242
 316 FAPSRFGTPEDLKSLIDRAHELGILVLMIDIVHSHSNNTLDGLNGFGDGTDTHTYFHGGR 375
 243 FAPSRFGTPEDLKSLIDRAHELGILVLMIDIVHSHSNNTLDGLNGFGDGTDTHTYFHGGR 302
 303 GHMMMDSRFLFNYSWEVLRLFLSNARWMLBEYKFDGFRPDGVTSMYTHGLOVFTN 362
 376 GHMMMDSRFLFNYSWEVLRLFLSNARWMLBEYKFDGFRPDGVTSMYTHGLOVFTN 435
 403 YHEYFGPATDVAVYVYLMVNDLHGLHPDVAISIGEDVSGMPTFCIPVDDGAVGDFYRLH 495
 436 YHEYFGPATDVAVYVYLMVNDLHGLHPDVAISIGEDVSGMPTFCIPVDDGAVGDFYRLH 422
 466 MAYAVADKTIWIELLKQSDSEWKGADIVHTLTNRRLWLEKCVTYAESHDQALVGDKTIAPFLMDK 555
 496 MAYAVADKTIWIELLKQSDSEWKGADIVHTLTNRRLWLEKCVTYAESHDQALVGDKTIAPFLMDK 582
 523 MAYAVADKTIWIELLKQSDSEWKGADIVHTLTNRRLWLEKCVTYAESHDQALVGDKTIAPFLMDK 592

QY 556 DMYDMLDRPSTPRIDRGIALHKMIRLVMTMGLGEGYLNFMGNEFGHPMIDFPRGPOT 615
 DB 483 DMYDMLANGPSTPRIDRGIALHKMIRLVMTMGLGEGYLNFMGNEFGHPMIDFPRGPOT 542
 QY 616 LPTGYLPGNNNSYDKCRREFDLDGADFLRYHGMQEFQAMOHLEEKYGMWTSBQYVSR 675
 DB 543 LPSGKFIPGNNNSYDKCRREFDLDGADFLRYHGMQEFQAMOHLEEKYGMWTSBQYVSR 602
 QY 676 KHEEKVILFEEDGDIYFVFNHNSFEDYRVCGRGKXKVALDSDALFGGFSRLDHD 735
 DB 603 KHEEDVIAFEKGDIVFVFNHNSFEDYRVCGRGKXKVALDSDALFGGFSRLDHD 662
 QY 736 VDYFTEHPHDNRPSFSVYTPSRTAVVYA 765
 DB 663 AEHTVSDCQHNRPHSFVYTPSRTAVVYA 692
 RESULT 7
 US-10-424-599-273691
 ; Sequence 273691, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 273691
 ; LENGTH: 870
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(870)
 ; LOCATION INFORMATION: unsure at all xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_89164C.1.pep
 US-10-424-599-273691
 Query Match 79.8%; Score 3325.5; DB 12; Length 870;
 Best Local Similarity 77.7%; Pred. No. 4.5e-303;
 Matches 600; Conservative 76; Mismatches 75; Indels 21; Gaps 5;
 QY 18 AAAQPELQIPEDIEQTAEV-NMTGTAELKESSEPT-----OG-IYETITD--- 63
 DB 74 SABLTPGLPDTSEDTQNLDEDTLMEDEKXNISEAASRYHIEDGGSVVSLVDVNI 133
 QY 64 -----GYTKVKEIVGBE--KRVVVKPGGQKTYEIDPTLKDFRSHLDYSEFRARA 116
 DB 134 PAKKASVVRKSKIVSDEVKPKXI PRPGTQKIYEIDPSLHNDHDLFRGQYKRLCY 193
 QY 117 AIOHHEGLAFAFGYKLGITRABGITYREMAFGAHSALVGFNNMNPADIMTRDD 176
 DB 194 EIDHHEGLTFSGKFGITRSATGITYREMAFGAHSALVGFNNMNPADIMTRNE 253
 QY 177 YGVWEIPLPNNADSPALPHGSRVKIRMDTPSGVDSISAMIKESVAPGSEIFNGIYD 236
 DB 254 FGWEIPLPNNVDSPIPHGSRVKIRMDTPSGIKDSIPAMIKESVAPGSEIPIYGIYD 313
 QY 237 PPEBEKVYFQHPQKRPBSGLIYSHIGMSPEPINSYANFRDVLVRIKSLGYNVQI 296
 DB 314 PPEBEKVYFQHPQKRPBSGLIYSHIGMSPEPINSYANFRDVLVRIKSLGYNVQI 373
 QY 297 MAIOEHSYVASFGYHVNFPFAPSGRFGTPEDLKSLIDRAHELGILVLDIVSHSSNNTL 356
 DB 374 MAIOEHSYVASFGYHVNFPFAPSGRFGTPEDLKSLIDRAHELGILVLDIVSHSSNNTL 433

QY 357 DGLNGFDGTDHYHFGGRGHHMMDSRLFNYSWEVLFLLSNNAWMLBEYKFDGRFD 416
 DB 434 DGLNMFDTGEGYFPRGSGYHMMDSRLFNYSWEVLFLLSNNAWMLDEYKFDGRFD 493
 QY 417 GVTSMYTHHGLQMTFTGNYGYPGPATVDVAVVYMLVNDLHGLAPDVSIGEDVSGM 476
 DB 494 GVTSMYTHHGLQMTFTGNYGYPGPATVDVAVVYMLVNDLHGLAPDVSIGEDVSGM 553
 QY 477 PFCIPVDGAGVSPYRLMAVADKMBILKOSDSWKGDIYHTLTNRMLEKVTYAE 536
 DB 554 PFCIPVDGAGVSPYRLMAVADKMBILKOSDSWKGDIYHTLTNRMLEKVTYAE 613
 QY 537 SHDQALVDGKTIAPMLDKMDYDFVALDPSFPRIDRGIALHKMIRLVMTMGLGEGYLNF 596
 DB 614 SHDQALVDGKTIAPMLDKMDYDFVALDPSFPRIDRGIALHKMIRLVMTMGLGEGYLNF 673
 QY 597 MGNRFGHEMIDFPRGPOTLPTGKYLPGNNNSYDKCRREFDLDGADFLRYHGMQEFQAM 656
 DB 674 MGNRFGHEMIDFPRGPOTLPTGKYLPGNNNSYDKCRREFDLDGADFLRYHGMQEFQAM 733
 QY 657 QHLEEKYGMWTSBQYVSRKHEEDKYLIFERDVLVFNHNSFEDYRVCGRGKXK 716
 DB 734 QHLEEKYGMWTSBQYVSRKHEEDKYLIFERDVLVFNHNSFEDYRVCGRGKXK 793
 QY 717 VALDSDALFGGFSRLDHDVYFTTEHPHDNRPSFSVYTPSRTAVVYALTE 768
 DB 794 IYLDSDDALFGGFSRLDHDVYFTTEHPHDNRPSFSVYTPSRTAVVYALAD 845
 RESULT 8
 US-10-254-534-2
 ; Sequence 2, Application US/10254534
 ; Publication No. US20030046730A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EK, Bo
 ; APPLICANT: KHOSNODI, Jamshid
 ; APPLICANT: LARSSON, Clas-Tomas
 ; APPLICANT: LARSSON, Hakan
 ; APPLICANT: RASK, Lars
 ; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
 ; FILE REFERENCE: 003300-486
 ; CURRENT APPLICATION NUMBER: US/10/254,534
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US/09/087,277
 ; PRIOR FILING DATE: 1998-05-29
 ; PRIOR APPLICATION NUMBER: PCT/SE96/01558
 ; PRIOR FILING DATE: 1996-11-28
 ; PRIOR APPLICATION NUMBER: SE 9504272-7
 ; PRIOR FILING DATE: 1995-11-29
 ; PRIOR APPLICATION NUMBER: SE 9601506-0
 ; PRIOR FILING DATE: 1996-04-19
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 878
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: bett gene (branching enzyme II)
 US-10-254-534-2
 Query Match 76.2%; Score 3175; DB 14; Length 878;
 Best Local Similarity 72.2%; Pred. No. 6.5e-289;
 Matches 583; Conservative 83; Mismatches 93; Indels 48; Gaps 6;
 QY 2 AIPFVSGATL--GVAPPAQPEHLOIP-----DIEQGTAE----- 37
 DB 60 STVAAGKVLVPTQSDSSSTQDFEFTTSBNSPASCTDVDSSTHNAQITENDV 119
 QY 38 ---VAMTGTAE-----XLESSEPTQGIYEITTDGYTKVKEIVGBEKPRAV 81
 DB 120 EBSSDLTGSEVLDFASSIQLOEGKLEBSKTLNTSETIITDESDR-IRE-----RGI 171


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QY      82 PKPGDQKYEIDPTLKDPRSHLDYRYSERYRIRAAIDQHEGGLAERGRYEKLGFTRSA 141
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      172 PPGGLGQKIYEIDPLNTNRHLDYRYSQYKRLBAIDKYEGGLEAFSRGKYMFTRSA 231
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      142 EGTTRERMAPGASALVGDENNPNADCTMTDDYGVWEIFLPNNAAGSPAIPIHGRYK 201
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      232 TGITREMAAGASALVGDENNPNADCTMTDDYGVWEIFLPNNAAGSPAIPIHGRYK 291
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      202 IRMDTSGVDSISAMIKESVOAGEIPENGIVYDPEEEKYVFQHPQPKRESRIYES 261
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      292 IRMDTSGVDSISAMIKESVOAGEIPENGIVYDPEEEKYVFQHPQPKRESRIYES 351
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      262 HIGMSSEPKINSYANFRDEVLPRIKLGYNVAVOIMAIQEHSYASFGYHTNFPAPSSR 321
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      352 HIGMSSEPKINSYANFRDEVLPRIKLGYNVAVOIMAIQEHSYASFGYHTNFPAPSSR 411
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      322 FGTPEDLKSLIDRAHEGLVLMQIVSHSSNNTLDGNGPDGDTYTHFGGPRGHMMW 381
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      412 FGXPDDKSLIDKAHEGLVLMQIVSHSSNNTLDGNGPDGDTYTHFGGPRGHMMW 471
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      382 DSRLENGSMEVLRFLSNARWMLBEEKYKFGDPGVTSMWYTHHGLQMTFTGNYGEYFG 441
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      472 DSRLENGSMEVLRFLSNARWMLBEEKYKFGDPGVTSMWYTHHGLQMTFTGNYGEYFG 531
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      442 FATVDVAVVYLMVNDLHGLHPDAVSIQEDVSGMPTFCIPVDGSGVGFYRLHNAVADK 501
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      532 LATVDVAVVYLMVNDLHGLHPDAVSIQEDVSGMPTFCIPVDGSGVGFYRLHNAVADK 591
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      502 WIELLKQSDSWKMGDIYHTLTNRRLKCYTYASHOALVGDXTIAFWLMDKMDYPM 561
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      592 WIELLKQSDSWKMGDIYHTLTNRRLKCYTYASHOALVGDXTIAFWLMDKMDYPM 651
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      562 ALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLNFMGNEFGHPMIDPRGQTLPTGYK 621
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      652 ALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLNFMGNEFGHPMIDPRGQTLPTGYK 711
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      622 LFGNNNSYDKCRRRFDLGDADFLRYHGMQEFDOAMQHLBEEKYGMTSEHQYVSRKHEBDK 681
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      712 LFGNNNSYDKCRRRFDLGDADFLRYHGMQEFDOAMQHLBEEKYGMTSEHQYVSRKHEBDK 771
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      682 VIFERGDVLFVNFHMSNPFDRYVCGSRPKRYKALDSDALFGGSRDLHDVDTFT 741
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      772 VIFERGDVLFVNFHMSNPFDRYVCGSRPKRYKALDSDALFGGSRDLHDVDTFT 831
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      742 EHPHNRPRSFSYTPSRTAUVYALTE 768
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      832 EGYWDRPRSIMYAPSRTAUVYALVD 858
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;

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RESULT 9
US-10-056-454A-15

; Sequence 15, Application US/10056454A
; Publication No. US20030166919A1

; GENERAL INFORMATION:

; APPLICANT: National Starch and Chemical Investment Holding Corporation
; TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:

; ADDRESSES: National Starch and Chemical Investment Holding Corporation
; STREET: 1000 Unigema Blvd.
; CITY: Newcastle
; STATE: Delaware
; COUNTRY: United States of America
; ZIP: 19720

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION NUMBER: US/10/056,454A
; FILING DATE: 25-Jun-2002
; INFORMATION FOR SEQ ID NO: 15:

```

;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 882 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-056-454A-15

```

Query Match 75.2%; Score 3135; DB 14; Length 882;
Best Local Similarity 71.4%; Pred. No. 3.8e-285;
Matches 576; Conservative 86; Mismatches 97; Indels 48; Gaps 6;

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QY      2 ATPVSGATL--GVAPPPAAQPEELQIP-----DIEQTAE----- 37
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      60 STVAASGKVLVGTQSDSSSTDOEFETSPENSPASTVDVSTHEASQIKTENDV 119
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      38 ---VAMTGTAT-----KLESEPTQGIYETITDGVTKVKELVGKEPRV 81
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      120 EBSDDLTSVEEDFASSLQLEGKLBESKTIANTSETIIDSER-IRE-----RGI 171
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      82 PKPGDQKYEIDPTLKDPRSHLDYRYSERYRIRAAIDQHEGGLAERGRYEKLGFTRSA 141
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      172 PPGGLGQKIYEIDPLNTNRHLDYRYSQYKRLBAIDKYEGGLEAFSRGKYMFTRSA 231
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      142 EGTTRERMAPGASALVGDENNPNADCTMTDDYGVWEIFLPNNAAGSPAIPIHGRYK 201
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      232 TGITREMAAGASALVGDENNPNADCTMTDDYGVWEIFLPNNAAGSPAIPIHGRYK 291
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      202 IRMDTSGVDSISAMIKESVOAGEIPENGIVYDPEEEKYVFQHPQPKRESRIYES 261
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      292 IRMDTSGVDSISAMIKESVOAGEIPENGIVYDPEEEKYVFQHPQPKRESRIYES 351
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      262 HIGMSSEPKINSYANFRDEVLPRIKLGYNVAVOIMAIQEHSYASFGYHTNFPAPSSR 321
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      352 HIGMSSEPKINSYANFRDEVLPRIKLGYNVAVOIMAIQEHSYASFGYHTNFPAPSSR 411
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      322 FGTPEDLKSLIDRAHEGLVLMQIVSHSSNNTLDGNGPDGDTYTHFGGPRGHMMW 381
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      412 FGTPEDLKSLIDRAHEGLVLMQIVSHSSNNTLDGNGPDGDTYTHFGGPRGHMMW 471
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      382 DSRLENGSMEVLRFLSNARWMLBEEKYKFGDPGVTSMWYTHHGLQMTFTGNYGEYFG 441
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      472 DSRLENGSMEVLRFLSNARWMLBEEKYKFGDPGVTSMWYTHHGLQMTFTGNYGEYFG 531
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      442 FATVDVAVVYLMVNDLHGLHPDAVSIQEDVSGMPTFCIPVDGSGVGFYRLHNAVADK 501
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      532 LATVDVAVVYLMVNDLHGLHPDAVSIQEDVSGMPTFCIPVDGSGVGFYRLHNAVADK 591
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      502 WIELLKQSDSWKMGDIYHTLTNRRLKCYTYASHOALVGDXTIAFWLMDKMDYPM 561
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      592 WIELLKQSDSWKMGDIYHTLTNRRLKCYTYASHOALVGDXTIAFWLMDKMDYPM 651
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      562 ALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLNFMGNEFGHPMIDPRGQTLPTGYK 621
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      652 ALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLNFMGNEFGHPMIDPRGQTLPTGYK 711
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      622 LFGNNNSYDKCRRRFDLGDADFLRYHGMQEFDOAMQHLBEEKYGMTSEHQYVSRKHEBDK 681
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      712 LFGNNNSYDKCRRRFDLGDADFLRYHGMQEFDOAMQHLBEEKYGMTSEHQYVSRKHEBDK 771
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      682 VIFERGDVLFVNFHMSNPFDRYVCGSRPKRYKALDSDALFGGSRDLHDVDTFT 741
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      772 VIFERGDVLFVNFHMSNPFDRYVCGSRPKRYKALDSDALFGGSRDLHDVDTFT 831
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
QY      742 EHPHNRPRSFSYTPSRTAUVYALTE 768
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;
Db      832 EGYWDRPRSIMYAPSRTAUVYALVD 858
;      ;      ;      ;      ;      ;      ;      ;      ;      ;      ;

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RESULT 10
US-10-254-534-4

; Sequence 4, Application US/10254534
; Publication No. US20030046730A1

```

; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT FILING DATE: 2002-09-26
; PRIOR FILING DATE: 1998-05-29
; PRIOR FILING DATE: 1998-05-29
; PRIOR FILING DATE: 1996-11-28
; PRIOR FILING DATE: 1996-11-28
; PRIOR FILING DATE: 1995-11-29
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:beli gene fragment (branching enz
; OTHER INFORMATION: co)
; US-10-254-534-4

Query Match      53.1%; Score 2213; DB 14; Length 464;
Best Local Similarity 86.0%; Pred. No. 7, 2e-199;
Matches 398; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

Cy 184 LPNNADGSPALPHGSRVKTIRMDTPSGVKSISAMIKFVSQAPSEIPNNGIYPPPESEKY 243
Db 1 LPNNADGSPALPHGSRVKTIRMDTPSGVKSISAMIKFVSQAPSEIPNNGIYPPPESEKY 60
Cy 244 VQGHQOPRPESELRITYESHIIGMSPPKINSYVNPDEVLPRFKRGYNVQVMAIOEHS 303
Db 61 IFQHRPKPKSLRIYESHIIGMSPPKINSYVNPDEVLPRFKRGYNVQVMAIOEHS 120
Cy 304 YYASFGYHVTNFPAPSSRFPTEDLKSLIDRAHELGLVLMIDIVSHSSNNTLDGLNGFD 363
Db 121 YYASFGYHVTNFXAPSSRFEXPDDKSLIDKAHELGLVLMIDIVSHSSNNTLDGLNMF 180
Cy 364 GTDTIYFHGSPRGHHMMWDSRLFNYSSEVLRFLSNARWMLBEYKFDGFRFGVTSMTY 423
Db 181 GTDSCYFHSAGAGYHMMWDSRLFNYSSEVLRFLSNARWMLBEYKFDGFRFGVTSMTY 240
Cy 424 THHGLOMTPTGNYGEYFPGFATVDVAVVYLMVNDLHGLHPDASVIGEDVSGMPTFCIPY 483
Db 241 THHGLSVGTGYEYEFGLATDVDAVYVLMVNDLHGLFPDAITIGEDVSGMPTFCIPY 300
Cy 484 PDGCVGFYRLHMAVADKWIILLKQSDSESWKMGDIVHTLTNRRLKCVTYAESHDQALY 543
Db 301 QDGGVGFYRLHMAVADKWIILLKQSDSESWKMGDIVHTLTNRRLKCVTYAESHDQALY 360
Cy 544 GDKTIAFWMLMDKMDPMDALDRPSTPRIDGIALHKKIRLVYTMGLGEGGLTNMGNEFGH 603
Db 361 GDKTIAFWMLMDKMDPMDALDRPSTPRIDGIALHKKIRLVYTMGLGEGGLTNMGNEFGH 420
Cy 604 PEMIDFPRGPOTLPFGKVLPGNNNSYDXXRRRRLDGDADFLRY 646
Db 421 PEMIDFPRAEQHLSDGSVLPNGNFSYDXXRRRRLDGDADFLRY 463

RESULT 11
US-10-336-753-56
; Sequence 56, Application US/10336753
; Publication No. US20030226176A1
; GENERAL INFORMATION:
; APPLICANT: Guan, Hanping
```

```

; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; FILE REFERENCE: 2461-52
; CURRENT FILING DATE: 2003-01-06
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1998-04-03
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Zea mays
; US-10-336-753-56

Query Match      51.5%; Score 2146; DB 12; Length 776;
Best Local Similarity 57.0%; Pred. No. 3, 3e-192;
Matches 395; Conservative 101; Mismatches 171; Indels 26; Gaps 6;

Cy 86 DQQKIYEIDPTLKDFRSHLDYRSEYRIRRAIDQHEGLEAFSRQYKLGFTRSAEGIT 145
Db 17 DHEIDYDDPFLKEIFKHFRYRMKRFLEQKSIENEGSLESFSKGYLKFGINTNEDGV 76
Cy 146 YREAPAGASALVGDPPNNPNMADYTRDDYGVYEIFLPNNADGSPALPHGSRVKTIRMD 205
Db 77 YREAPAPAOEMLIGDFNDMGNANKMEKDKFGVMSIKI-DHVKGKPALPHNSKVAFRL 135
Cy 206 TPSSVKOSISAMIKFVSQAPSEI--PFGIYVDPPEEEKYVQHPQPKPESLRITYESHI 263
Db 136 HGVWVDRIPRLIRKATYDASKFGAPYDGVKHPDASERYTTKHPRSPAPRILEAVY 195
Cy 264 GMSPPKINSYVNPDEVLPRFKRGYNVQVMAIOEHSYYASFGYHVTNFPAPSSRF 323
Db 196 GMSSEKPAVSYTRFADAVLPRIRANNYNTVQVMAIWEHSYYASFGYHVTNFPAPSSRF 255
Cy 324 TPEDLKSLIDRAHELGLVLMIDIVSHSSNNTLDGLNGFD--GDDTHFHGSPRGHHMM 380
Db 256 TPEDLKSLIDRAHSLIGRLVMDVSHSSNNTDGLNGDVQSIOESYFHAQDRGYHKL 315
Cy 381 WDSRLFNYSSEVLRFLSNARWMLBEYKFDGFRDGYVTSMTYTHHGLOMTPTGNYGEYF 440
Db 316 WDSRLFNYSSEVLRFLSNARWMLBEYKFDGFRDGYVTSMTYTHHGLOMTPTGNYGEYF 375
Cy 441 GFATVDVAVVYLMVNDLHGLHPDASVIGEDVSGMPTFCIPVDPGCVGFYRLHMAVAD 500
Db 376 SLDAVAVVYVYMLANHLMEKLLPEATVVAEVSQMPVLCRPVDSGVGFYRLHMAVAD 435
Cy 501 KWILLKQSDDS--KMGDIVHTLTNRRLKCVTYAESHDQALYDGTIAFWMLMDKMDYD 559
Db 436 KWILLKQSDSESMGSIATLTNRRTYKTIASHSDDOIVGDKTIAFWMLMDKMDYD 495
Cy 560 FMAIDRSTPRIDGIALHKKIRLVYTMGLGEGGLTNMGNEFGHPEMIDFPRGPOTLPFG 619
Db 496 GMSDLOQSPSTIDGIALQKMIHFTMALGGDGYLTFNGNEFGHPEMIDFPR----- 547
Cy 620 KVLPGNNNSYDXXRRRRLDGDADFLRYHGMQEFDOAQHLEKYGFTSEHQYVSKHEE 679
Db 548 ---EGNNWSYDXXRRRRLDGDADFLRYHGMQEFDOAQHLEKYGFTSEHQYVSKHEE 604
Cy 680 DKVLIIPERGLVVFNFHMSNSFPDYRGSGHPGYKVALDSDDLFGGFSRLDHDVDYF 729
Db 605 EKVIIFERGLVVFNFHMSNSFPDYRGSGHPGYKVALDSDDLFGGFSRLDHDVDYF 664
Cy 740 TT-----EHPDNRPSFSVYTPSRVAVY 764
Db 665 TSPEGVGVPEPTNFRNRSFKVLSPPRTCVAY 697
```


Db 590 ETRFNRRPNSFKVLSPRTCVAY 612

RESULT 14

US-10-369-493-3969
Sequence 3969, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3969
LENGTH: 874
TYPE: PRT
ORGANISM: Neurospora crassa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(874)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3969

Query Match 46.0%; Score 1917.5; DB 15; Length 874;
Best Local Similarity 46.8%; Pred. No. 1.2e-170;
Matches 378; Conservative 109; Mismatches 185; Indels 135; Gaps 11;

QY 81 VPKRGGQKLY-----EIDPTLKDRSHLDVYSEYRRIAD 119
DB 23 IPKDGMSLYIRFSLPIQCKLIKAGVLSIDPMLRPPKDLKSRQASQSIDITIN 82
QY 120 OHEGGLAERF-----GYEKLGTRSAEG-ITYREMAFGASAL 158
DB 83 KTEGGLEKFSRVGSXAALMTLPKLLTHVQLGTEIFGVNDKONTITRENAAPNAKQSL 142
QY 159 VEDFN-----NPNADTYTRDDYGYWEFLPNADGSPAIPIQS 198
DB 143 IGFSTYHDTTPRYCELGATLTLRLQWRNARKKIEFGVEITIPETAGOPAIPIQS 202
QY 199 RVK-----IRMDTPSGV-KDSISAWIKPSVQAPGEIP-ENG 232
DB 203 KIKVCECNFSACTPIRHANVLMFISKQITTELPDQWDRIPAMIKYTTQDLSVPAVEA 262
QY 233 IYDPEEEXKVFQHPQKRPESLRIYESHIGNSPEPKINSYANFRDEVLPRIKLQYN 292
DB 263 RFNPNPQSEKTYFKHKRPSKPESLRIYEAHVIGISSPEKVAITYEFKTMIPRIKILQYN 322
QY 293 AVOIMAIQESHYASFGHYNTNFPASSRFGTPEDLKSLIRARLEGLVLMQIVHSSS 352
DB 323 AIQIMAIMERAYYASFGYQVNSFPASSRFGTPEDLKSLIRARLEGLVLMQIVHSSS 382
QY 353 NNTLDGNGSDGUDTHFEHGGPRGHHMMWDBRLFNYSWEVLRFLLSARWMLSEYKPDG 412
DB 383 KAVLDGNEEDGDHOFHGGGRGKDLMDSRLLPNYGHHEMRRLSLRWMWMBETAYDGS 442
QY 413 FRDGVTSMTYTHGLQMT-----FTNGYGEYFGATDVDAVYIMLV 455
DB 443 FRDGVTSMTYTHGLQMT-----FTNGYGEYFGATDVDAVYIMLV 455
QY 456 NDILHGLHPRAVSIEGVSGMPTFCIPVDGCGVDFRILMAVADKMTLLKQ--SDSEWK 514
DB 503 NENLHOLYPRVITVAEDVSGMPALCLPLSGVGDFYRLAALIDPMIKILKEKDESD 562
QY 515 MGDIVATLTRRMLEKCVTAESHDAQ-----LVGDKTIAFWLMDXD 556

Db 563 MANITWLTNRHGEKTIAYCESHDQAVTYTPATCSGXRNRRLVGDXTLMMHLCDAB 622
QY 557 MYDFMALDRPSTPRIDRGIALHKMIRLVTMGCGEGYIAFMGNREHPEMIDPRRGQTL 616
DB 623 LYTNMSILTPLPVIDRGVALHKMIRLTHSLGSGEYLNPEGNHFGPEWLDPR----- 677
QY 617 PTGKVLPGNNNSYDCORRPFIDGADFLRYHGWQEDQAMQHEEKYGFMTSEHQYYSRK 676
DB 678 -----EGQNSFWTARRQNLTEGCLRYQYIANFDRSNMLTEKYGMLHAPQAYISLK 731
QY 677 HEEDVLIIFERGLVFPVFNHMSNPFDDYRVGCSRPKTKVALDSDALFGFSRLDDHV 736
DB 732 HEGDKVIFERAGLVFVFNHMSNPFDDYRVGCSRPKTKVALDSDALFGFSRLDDHV 736
QY 737 DYFTTEHPHNRPRPSVYTPSRTAVY 763
DB 792 RFTSDLPNNRKNSTHYIIPARTAV 818

RESULT 15

US-10-425-114-45676
Sequence 45676, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack B.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 45676
LENGTH: 421
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700747645_FLI.pep
US-10-425-114-45676

Query Match 45.9%; Score 1915; DB 12; Length 421;
Best Local Similarity 84.1%; Pred. No. 6.7e-171;
Matches 333; Conservative 38; Mismatches 25; Indels 0; Gaps 0;

QY 373 GPRGHMMWDSRLFNYSWEVLRFLSNARWMLSEYKPDGFRDGVTSMTYTHGLQMTF 432
DB 1 GSRGTHMMWDSRLFNYSWEVLRFLSNARWMLSEYKPDGFRDGVTSMTYTHGLQMTF 60
QY 433 TGNVGEYFGFATDVAVYIMLVNDLHGLHDPVAVSIEGDSGMPPTFCIPVDGCGVFDY 492
DB 61 TGNVGEYFGFATDVAVYIMLVNDLHGLHDPVAVSIEGDSGMPPTFCIPVDGCGVFDY 120
QY 493 RILMAVADKMTLLKQSDSSTKGGDVTHTLTRRMLEKCTYAESHDQALVGDKTIAFWL 552
DB 121 RILMAVADKMTLLKQSDSSTKGGDVTHTLTRRMLEKCTYAESHDQALVGDKTIAFWL 180
QY 553 MDKQVDFMALDRPSTPRIDRGIALHKMIRLVTMGCGEGYIAFMGNREHPEMIDPRRG 612
DB 181 MDKQVDFMALDRPSTPRIDRGIALHKMIRLVTMGCGEGYIAFMGNREHPEMIDPRRG 240
QY 613 PQLPPTGKVLPGNNNSYDCORRPFIDGADFLRYHGWQEDQAMQHEEKYGFMTSEHQY 672
DB 241 PQLPPTGKVLPGNNNSYDCORRPFIDGADFLRYHGWQEDQAMQHEEKYGFMTSEHQY 672
QY 673 VSRKNEEDKVIIFERAGLVFVFNHMSNPFDDYRVGCSRPKTKVALDSDALFGFSRL 732
DB 301 VSRKNEEDKVIIFERAGLVFVFNHMSNPFDDYRVGCSRPKTKVALDSDALFGFSRL 732
QY 733 DHDVDYFTTEHPHNRPRPSVYTPSRTAVYALTE 766

Tue Apr 20 10:02:28 2004

us-09-508-377-12.rapb

Page 10

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      :| :|||:| :|:||||| :| ||||| ||||| :
Db 361 NHTAEYFTSEGWYDDRRPSFLIYAPSRTAVVYALAD 396

```

Search completed: April 15, 2004, 08:44:07
Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 08:35:16 ; Search time 21 Seconds
(without alignments)

3517,862 Million cell updates/sec

Title: US-09-508-377-12

Perfect score: 4169
Sequence: 1 MATFAVSGATLGVARPPAA.....PRSSVTTPSRATVVALTE 768

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pinned, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4113.5	98.7	823	2 T06574	probable 1,4-alpha
2	3915	93.9	729	2 T06797	1,4-alpha-glucan b
3	3588.5	86.1	814	2 T02041	starch branching e
4	3362	80.6	825	2 A48537	1,4-alpha-glucan b
5	3351	80.4	799	2 T01653	1,4-alpha-glucan b
6	3346	80.3	922	2 T06453	1,4-alpha-glucan b
7	3342	80.2	799	2 T02981	1,4-alpha-glucan b
8	3258	78.1	800	2 S65046	1,4-alpha-glucan b
9	3258	78.1	805	2 T48392	1,4-alpha-glucan b
10	3207	75.9	830	2 T07743	probable 1,4-alpha
11	3155	75.7	858	2 B84780	starch branching e
12	3135	75.2	854	2 S65045	1,4-alpha-glucan b
13	2193.5	52.6	830	2 T06578	1,4-alpha-glucan b
14	2168.5	52.0	830	2 T07824	1,4-alpha-glucan b
15	2166.5	52.0	820	1 JX0243	1,4-alpha-glucan b
16	2146	51.5	822	2 UJ0968	1,4-alpha-glucan b
17	2140	51.3	702	2 A46075	1,4-alpha-glucan b
18	2122.5	50.9	861	1 S34730	1,4-alpha-glucan b
19	2099.5	48.6	826	2 T06494	1,4-alpha-glucan b
20	2027.5	45.5	733	2 T49679	probable branching
21	1896	45.5	681	2 T42426	hypothetical prote
22	1795.5	43.1	704	1 S50448	1,4-alpha-glucan b
23	1494	35.8	686	1 T06334	1,4-alpha-glucan b
24	1048	25.1	383	2 S28422	1,4-alpha-glucan b
25	624	15.0	774	1 UQ0550	1,4-alpha-glucan b
26	592.5	14.2	666	1 D82511	1,4-alpha-glucan b
27	573	13.7	770	2 S76095	hypothetical prote
28	562	13.5	764	2 AG1895	1,4-alpha-glucan b
29	558	13.4	730	1 I64118	1,4-alpha-glucan b

30	554	13.3	727	2 AH0479	1,4-alpha-glucan b
31	553.5	13.3	728	1 NO8CA	1,4-alpha-glucan b
32	550.5	13.2	705	2 D75345	probable 1,4-alpha
33	550.5	13.2	728	2 E91163	1,4-alpha-glucan b
34	550.5	13.2	728	2 F86009	1,4-alpha-glucan b
35	549.5	13.2	630	2 D70363	1,4-alpha-glucan b
36	548.5	13.2	728	2 AF0995	1,4-alpha-glucan b
37	548	13.1	735	2 AH3057	glycogen branching
38	548	13.1	735	2 F98228	1,4-alpha-glucan b
39	540.5	13.0	666	2 B56639	1,4-alpha-glucan b
40	540	13.0	638	2 S18599	1,4-alpha-glucan b
41	537	12.9	732	2 H83376	1,4-alpha-glucan b
42	529	12.7	731	2 UC7919	1,4-alpha-glucan b
43	525.5	12.6	731	2 B70770	probable 91gB prot
44	521	12.5	639	1 B41328	1,4-alpha-glucan b
45	517.5	12.4	737	2 C81724	1,4-alpha-glucan b

ALIGNMENTS

```
RESULT 1
T06574
probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) II precursor - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C:Accession: T06574
R:Chldbat, R.N.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z15769
A:Accession: T06574
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-823 <CH>
A:Cross-references: EMBL:Y11282; PIDN:CAA72154.1
A:Experimental source: cv. Fielder; kernels 12 days post anthesis
C:Genetics:
A:Gene: sbe2
C:Function:
A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-
A:Pathway: glycogen/starch biosynthesis
C:Superfamily: 1,4-alpha-glucan branching enzyme
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
F:1-55/Domain: transit peptide (amyloplast) #status predicted <TNP>
F:55-823/Product: 1,4-alpha-glucan branching enzyme II #status predicted <MAT>

Query Match          98.7%; Score 4113.5; DB 2; Length 823;
Best Local Similarity 93.0%; Pred. No. 2.5e-301;
Matches 765; Conservative 0; Mismatches 3; Indels 55; Gaps 1;

QY      1 MATFAVSGATLGVARPPAA-----
DB      1 MATFAVSGATLGVARPPAGGGLPRSGSERGGVDIPSLLRKXSSRAVLSAASGK 60
QY      20 -----AQPETLQIPEDIEBQTAENVMTGTAEKLESSSEPTQIVETITDGV 65
DB      61 VLVPDGSDDLASPAPELQITPEDIEBQTAENVMTGTAEKLESSSEPTQIVETITDGV 120
QY      66 TNGVKELVVEKERVVFKPDGGKIYEIDPTLQDFRSHLDYRSEYRIRAIIDQHEGGL 125
DB      121 TNGVKELVVEKERVVFKPDGGKIYEIDPTLQDFRSHLDYRSEYRIRAIIDQHEGGL 180
QY      126 EAFSRGKYELGFRSAEGITTYREMAPGNSAALVGDNNMNPNDITMRDYGWEITLP 185
DB      181 EAFSRGKYELGFRSAEGITTYREMAPGNSAALVGDNNMNPNDITMRDYGWEITLP 240
QY      186 NNADGSPALPHGSRVRIKMDTPSGVDSISAWIKFSVQADGELPFNGIYYDPPESEKTVF 245
DB      241 NNADGSPALPHGSRVRIKMDTPSGVDSISAWIKFSVQADGELPFNGIYYDPPESEKTVF 300
QY      246 QHPQPRPSRLRIYESHIGNSPEPKINSYANRDEVLPIKILGVNAVQMAIQEHSY 305
DB      301 QHPQPRPSRLRIYESHIGNSPEPKINSYANRDEVLPIKILGVNAVQMAIQEHSY 360
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QY 306 ASFGYHTNFPAPSSRFGTPEDLKSLIDRAHELGLVLMIDIVSHSSNNTLDGLNGFDGT 365
 DB 361 ASFGYHTNFPAPSSRFGTPEDLKSLIDRAHELGLVLMIDIVSHSSNNTLDGLNGFDGT 420
 QY 366 DTHYFHGGPRGHMMWDSRLFNYSWEVLRFLSNARWMLBEYKDFGDFGVTSMYTH 425
 DB 421 DTHYFHGGPRGHMMWDSRLFNYSWEVLRFLSNARWMLBEYKDFGDFGVTSMYTH 480
 QY 426 HGLQMTTGNNGEYFGFATDVAVYYLMLVNDLHGLHPDASIGEDVSGMTFCIPVD 485
 DB 481 HGLQMTTGNNGEYFGFATDVAVYYLMLVNDLHGLHPDASIGEDVSGMTFCIPVD 540
 QY 486 GGVPFDRLHMAVADKMTLELKQSDSWMGDIYHTLTNRRLKCVTAESHDOALVGD 545
 DB 541 GGVPFDRLHMAVADKMTLELKQSDSWMGDIYHTLTNRRLKCVTAESHDOALVGD 600
 QY 546 KTIAPWIMDKMYDFMALDRPSTPRIDRGIALHKXIRLVTMGLGEGYLNFMNGEFGHE 605
 DB 601 KTIAPWIMDKMYDFMALDRPSTPRIDRGIALHKXIRLVTMGLGEGYLNFMNGEFGHE 660
 QY 606 WIDPPRGQTLPTGKVLFGNNNSYDKCRRRPDLGDADFLRYHGMQEFDDAMHLEBKXGF 665
 DB 661 WIDPPRGQTLPTGKVLFGNNNSYDKCRRRPDLGDADFLRYHGMQEFDDAMHLEBKXGF 720
 QY 666 MTSEHOVYSRKHEEDKVIIFERGDIVFVNFHMSNSFFDYRGCSRPGRKYVALDSDAL 725
 DB 721 MTSEHOVYSRKHEEDKVIIFERGDIVFVNFHMSNSFFDYRGCSRPGRKYVALDSDAL 780
 QY 726 FGGSRLDHDVDYFTTEHPDNRPRSFSVYTPSRJAVVYALTE 768
 DB 781 FGGSRLDHDVDYFTTEHPDNRPRSFSVYTPSRJAVVYALTE 823

RESULT 2

106797
 probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - wheat
 N:Alternate names: 1,4-alpha-D-glucan 6-alpha-D-(1,4)-alpha-D-glucanotransferase
 C:Species: Triticum aestivum (common wheat)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 18-Jun-1999
 C/Accession: T06797
 R:Koegeer, C.; Loez, H.; Juetlicke, S.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z15822
 A/Accession: T06797
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-729 <KRC>
 A/Cross-references: EMBL:U66376; NID:g1620661; PIRN:AA017086.1; PID:g1620662
 A/Experimental source: cv. Florida; kernels 21 DAP
 C/Function:
 A:Description: converts amylose into amylopectin; catalyzes the formation of 1,6-glucose
 A/Pathway: starch and sucrose metabolism
 C:Superfamily: 1,4-alpha-glucan branching enzyme
 C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 93.9%; Score 3915; DB 2; Length 729;
 Best Local Similarity 98.2%; Pred. No. 1.8e-286;
 Matches 716; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 40 MTGTAELKESSEPTGIVETITDGTGKVELVGEKPRVVPKPGDGKIVEIDPTLKD 99
 DB 1 MTGTAELKESSEPTGIVETITDGTGKVELVGEKPRVVPKPGDGKIVEIDPTLKD 60
 QY 100 FRSHLDYRSEYKRIAPALDQEGLEAFSRGTEKGFTRSAEGITRYEWAAPGAHSAIV 159
 DB 61 FRSHLDYRSEYKRIAPALDQEGLEAFSRGTEKGFTRSAEGITRYEWAAPGAHSAIV 120
 QY 160 GPNMNNPAAQMTPTDYGWVEIFLNNMADGSPAIRHGSVYKIRMPDPSGVKDSISAMIK 219
 DB 121 GPNMNNPAAQMTPTDYGWVEIFLNNMADGSPAIRHGSVYKIRMPDPSGVKDSISAMIK 180
 QY 220 FSVQAPGEIPFNGIYDPEEKEKVFQHPQKRPESLRIYESHIGMSSPEPKINSYANFR 279

DB 181 FSVQAPGEIPFNGIYDPEEKEKVFQHPQKRPESLRIYESHIGMSSPEPKINSYANFR 240
 QY 280 DEVLPRIKLGVAVOIMAIQESHYYASFGYHTNFPAPSSRFGTPEDLKSLIDRAHBLG 339
 DB 241 DEVLPRIKLGVAVOIMAIQESHYYASFGYHTNFPAPSSRFGTPEDLKSLIDRAHBLG 300
 QY 340 LVLAMDIVSHSSNNTLDGLNGFDGIDTHYFHGGPRGHMMWDSRLFNYSWEVLRFLLS 399
 DB 301 LVLAMDIVSHSSNNTLDGLNGFDGIDTHYFHGGPRGHMMWDSRLFNYSWEVLRFLLS 360
 QY 400 NARWMLBEYKDFGDFGVTSMYTHHGLQMTTGNNGEYFGFATDVAVYYLMLVNDLI 459
 DB 361 NARWMLBEYKDFGDFGVTSMYTHHGLQMTTGNNGEYFGFATDVAVYYLMLVNDLI 420
 QY 460 HGLHPDASIGEDVSGMTFCIPVDGVPDRLHMAVADKMTLELKQSDSWMGDIY 519
 DB 421 HGLHPDASIGEDVSGMTFCIPVDGVPDRLHMAVADKMTLELKQSDSWMGDIY 480
 QY 520 HTLTNRRLKCVTAESHDOALVGDKTIAPWIMDKMYDFMALDRPSTPRIDRGIALHK 579
 DB 481 HTLTNRRLKCVTAESHDOALVGDKTIAPWIMDKMYDFMALDRPSTPRIDRGIALHK 540
 QY 580 MRLVTMGLGEGYLNFMNGEFGHEWIDPPRGQTLPTGKVLFGNNNSYDKCRRRPDLG 639
 DB 541 MRLVTMGLGEGYLNFMNGEFGHEWIDPPRGQTLPTGKVLFGNNNSYDKCRRRPDLG 600
 QY 640 DAPFLRYHGMQEFDDAMHLEBKXGFMTSEHOVYSRKHEEDKVIIFERGDIVFVNFHMS 699
 DB 601 DAPFLRYHGMQEFDDAMHLEBKXGFMTSEHOVYSRKHEEDKVIIFERGDIVFVNFHMS 660
 QY 700 NSFEDYVVGCSRPGRKYVALDSDALFGGSRLDHDVDYFTTEHPDNRPRSFSVYTPSR 759
 DB 661 NSFEDYVVGCSRPGRKYVALDSDALFGGSRLDHDVDYFTTEHPDNRPRSFSVYTPSR 720
 QY 760 TAVVYALTE 768
 DB 721 TAVVYALTE 729

RESULT 3

102041
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) Iia - maize (fragment)
 N:Alternate names: starch branching enzyme Iia
 C:Species: Zea mays (maize)
 C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 18-Jun-1999
 C/Accession: T02041
 R:Go, M.; Fisher, D.K.; Kim, K.N.; Shannon, J.C.; Gaultman, M.J.
 Plant Physiol. 114, 69-78, 1997
 A>Title: Independent genetic control of maize starch-branching enzymes Iia and Iib. Is
 A:Reference number: Z14509; MUID:97303618; PMID:9159942
 A/Accession: T02041
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-814 <GAO>
 A/Cross-references: EMBL:U65948; NID:G2340107; PIRN:AA067316.1; PID:G2340108
 A/Experimental source: strain B73
 C/Genetics:
 A/Gene: Sbe2a
 C/Function:
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D
 A/Pathway: glycogen/starch biosynthesis
 C:Superfamily: 1,4-alpha-glucan branching enzyme
 C/Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 86.1%; Score 3588.5; DB 2; Length 814;
 Best Local Similarity 84.7%; Pred. No. 8.4e-262;
 Matches 662; Conservative 32; Mismatches 49; Indels 39; Gaps 4;

QY 11 LGVAPPAAGPEELQIPEDIEQTAEVNMGTAELKESSEPTG----- 55
 DB 38 LSSAEPVVDTPQELQIPE-----AEI-----TYEK-TSSSPDTQTSVAVAASSGVEAE 85

QY 56 -----GIVETITDVTGKVELVGEKPRVVERPGDQKIYEIDPTLKDFRSH 103
 DB ERPELSEVIGVGGTGTGKIDGAKAKAPLVEEKPRVIPPBGDGRITYEIDPTLGEFRGH 145
 QY 104 LDYRSEVRRIAPADQHEGGLEAFSRGVEKIGFTTSAGGITRYEMAPGASALVGDEN 163
 DB 146 LDYRSEVRRIAPADQHEGGLEAFSRGVEKIGFTTSAGGITRYEMAPGASALVGDEN 205
 QY 164 NNNPAPADMTDNDYGVWEIPLNNADGSPALPHSGSVKIRMDTPSGKDSISAMIKFSVQ 223
 DB NNNPAPADMTDNDYGVWEIPLNNADGSPALPHSGSVKIRMDTPSGKDSISAMIKFSVQ 265
 QY 224 APGEIPIYNGIYDPPPEEKYVFQHPQKPRPESIRIYESHIGMSPEPKINSVANFDEVL 283
 DB 266 APGEIPIYNGIYDPPPEEKYVFQHPQKPRPESIRIYESHIGMSPEPKINTYANFDEVL 325
 QY 284 PRIRKLGYNVAVOIMAIQESHYSYASFGYHVTNFPAPSSRFGTPEDLKSLIDRAHELGILV 343
 DB 326 PRIRKLGYNVAVOIMAIQESHYSYASFGYHVTNFPAPSSRFGTPEDLKSLIDRAHELGILV 385
 QY 344 MDIVSHSSNNTLDGLNGFDGTDTHYFHGGPRGHHMMMDSRLFNYSGWELRFLLSNARV 403
 DB 386 MDIVSHSSNNTLDGLNGFDGTDTHYFHGGPRGHHMMMDSRLFNYSGWELRFLLSNARV 445
 QY 404 WLEBYKFDGFRDGYTSMYTHHGLQMTFTGNIGYFEGATDVDAVYVLMVNDLIHGLH 463
 DB 446 WLEBYKFDGFRDGYTSMYTHHGLQMTFTGNIGYFEGATDVDAVYVLMVNDLIHGLH 505
 QY 464 PDVAVSIGEVSGMPFICIPVDPGGVGFYRLHMAVADKMTIELLKQSBESKMGDIYHTLT 523
 DB 506 PEAVSIGEVSGMPFICIPVDPGGVGFYRLHMAVADKMTIELLKQSBESKMGDIYHTLT 565
 QY 524 NRRMLEKCTVYAESHDQALVGDKTIAFWMMDKMDYFMALDRPSTPRIDGIALHMKIRL 583
 DB 566 NRRMLEKCTVYAESHDQALVGDKTIAFWMMDKMDYFMALDRPSTPRIDGIALHMKIRL 625
 QY 584 VTMGLGEGCYLNFNGNEFGHPWIDFPBGPQPLPTGKVLPGNNNSYDKCRRRFDLGDAD 643
 DB 626 VTMGLGEGCYLNFNGNEFGHPWIDFPBGPQPLPTGKVLPGNNNSYDKCRRRFDLGDAD 685
 QY 644 LRYHMOEFDQAMOHLEEKYGFTSEHYYSRCHGEBKXIIIFERGDVVFENFHMSSSF 703
 DB 686 LRYHMOEFDQAMOHLEEKYGFTSEHYYSRCHGEBKXIIIFERGDVVFENFHMSSSF 745
 QY 704 DYRVGCSRGKTKYVALDSDDALFGGFSRLDHDVDYFTEHPPHNRPRSPFYVTPSRVAV 763
 DB 746 DYRVGCSRGKTKYVALDSDDALFGGFSRLDHDVDYFTEHPPHNRPRSPFYVTPSRVAV 805
 QY 764 YV 765
 DB 806 YV 807
 RESULT 4
 A48537
 starch branching enzyme isoform RBE3 - rice
 C:Species: Oryza sativa (rice)
 C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
 C:Accession: A48537
 R:Mituno, K.; Kawasaki, T.; Shimada, H.; Sato, H.; Kobayashi, E.; Okumura, S.; Arai, Y.
 J. Biol. Chem. 268, 19084-19091, 1993
 A:Title: Alteration of the structural properties of starch components by the lack of an
 A:Reference number: A48537, PMID:9336883, PMID:8360192
 A:Accession: A48537
 A:Status: preliminary
 A:Molecule type: mRNA, protein
 A:Residues: 1-825 <M12>
 A:Cross-references: GB:D16201; NID:G336051; PIDN:BAAC3738.1; PID:G436052
 A:Experimental source: CV, Kilmaze
 A:Note: sequence extracted from NCBI backbone (NCBIN:136747, NCBI:P.136748)
 C:Superfamily: 1,4-alpha-glucan branching enzyme
 Query Match 80.6%; Score 3362; DB 2; Length 825;

Best Local Similarity 80.1%; Pred. No. 9.7e-245;
 Matches 602; Conservative 68; Mismatches 72; Indels 10; Gaps 2;
 QY 17 PAAAPPELQIPEDIEBQTAENMTGTAEKLESEPPQGIETITDVTGKVELVGE 76
 DB 84 PVAAGSDDLQPLADDELSTEV-----GAVEIIESSGAD-----VEGKRYVEELAAQ 133
 QY 77 KPRVVPKGGQKIYEIDPTLKDFRSHLDYRSEVRRIAPADQHEGGLEAFSRGVEKIG 136
 DB 134 KPRVVPKGGQKIYFQDMSMLNGYKHLEYRYSILYRLRSIDIDQYEGGLETSRGEKIG 193
 QY 137 PTRABEGITRYEMAPGASALVGDENNNNPNADMTDDVGVMTFLPNNADGSPALPH 196
 DB 194 FNSHAGVTRYEMAPGASALVGDENNNNPNADMTDDVGVMTFLPNNADGSPALPH 253
 QY 197 GSRVYKIRMDTPSGKDSISAMIKFSVQAPGEIPIYNGIYDPPPEEKYVFQHPQKPRPES 256
 DB 254 GSRVYKIRMDTPSGKDSISAMIKFSVQAPGEIPIYNGIYDPPPEEKYVFQHPQKPRPES 313
 QY 257 RYESHIGMSPEPKINSVANFDEVLPRIRKLGYNVAVOIMAIQESHYSYASFGYHVTNFP 316
 DB 314 RYESHIGMSPEPKINTYANFDEVLPRIRKLGYNVAVOIMAIQESHYSYASFGYHVTNFP 373
 QY 317 APSSRFGTPEDLKSLIDRAHELGILVMDIVSHSSNNTLDGLNGFDGTDTHYFHGGPRG 376
 DB 374 APSSRFGTPEDLKSLIDRAHELGILVMDIVSHSSNNTLDGLNGFDGTDTHYFHGGPRG 433
 QY 377 HHHMMDSRLFNYSGWELRFLLSNARVWLEBYKFDGFRDGYTSMYTHHGLQMTFTGNV 436
 DB 434 HHHMMDSRLFNYSGWELRFLLSNARVWLEBYKFDGFRDGYTSMYTHHGLQMTFTGNV 493
 QY 437 GEYGFATDVDAVYVLMVNDLIHGLHDAVSGISGDSMPFICIPVDPGGVGFYRLHM 496
 DB 494 SEYGFATDVDAVYVLMVNDLIHGLHDAVSGISGDSMPFICIPVDPGGVGFYRLHM 553
 QY 497 AVADKMTIELLKQSBESKMGDIYHTLTNRRMLEKCTVYAESHDQALVGDKTIAFWMMDK 556
 DB 554 AVADKMTIELLKQSBESKMGDIYHTLTNRRMLEKCTVYAESHDQALVGDKTIAFWMMDK 613
 QY 557 MYDFMALDRPSTPRIDGIALHMKIRLVTMGAGGEGYLNFMNGNEFGHPWIDFPBGPQPL 616
 DB 614 MYDFMALDRPSTPRIDGIALHMKIRLVTMGAGGEGYLNFMNGNEFGHPWIDFPBGPQPL 673
 QY 617 PTGKVLPGNNNSYDKCRRRFDLGDADFLRYHMOEFDQAMOHLEEKYGFTSEHYYSRK 676
 DB 674 PNGKFIPIGNNSYDKCRRRFDLGDADFLRYHMOEFDQAMOHLEEKYGFTSEHYYSRK 733
 QY 677 HEEDKVIIFERGDVVFENFHMSSNFPDYRVGCSRGKTKYVALDSDDALFGGFSRLDHDV 736
 DB 734 HEEDKVIIFERGDVVFENFHMSSNFPDYRVGCSRGKTKYVALDSDDALFGGFSRLDHDV 793
 QY 737 DYFTEHPPHNRPRSPFYVTPSRVAVYALTE 768
 DB 794 EHFADCSHNRPRSPFYVTPSRVAVYALTE 825
 RESULT 5
 T01663
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) IIB - maize
 N:Alternate names: starch branching enzyme IIB
 C:Species: Zea mays (maize)
 C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 18-Jun-1999
 C:Accession: T01663
 R:Kim, K.N.; Fisher, D.K.; Gao, M.; Guiltinan, M.J.
 submitted to the EMBL Data Library, June 1998
 A:Description: Molecular cloning and characterization of the amylose-extender gene enco
 A:Reference number: Z4387
 A:Accession: T01663
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-799 <KIM>
 A:Cross-references: EMBL:AF072725; NID:G3511235; PIDN:AA03764.1; PID:G3511236
 A:Experimental source: strain B73

C:Genetics: ae
A:Introns: 38/1; 86/3; 138/2; 171/2; 185/3; 205/3; 232/3; 271/3; 299/3; 340/2; 360/2; 424/2
C:Function: C
A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-galactose
A:Pathway: glycosyl transferase
C:Superfamily: 1,4-alpha-glucan branching enzyme
C:Keywords: glycosyl transferase; hexosyltransferase; glycosyltransferase; hexosyltransferase

Query Match 80.4%; Score 3351; DB 2; Length 799;
Best Local Similarity 78.5%; Pred. No. 6.2e-244;
Matches 609; Conservative 68; Mismatches 77; Indels 22; Gaps 4;

OY 4 FAVSAGTLCV-----APPAAAPPELQIPDIEBQTAENVNNTGGAEKLESE----- 52
DB 35 FLTRGRVGGSGTHGARAAARAAKAAVWPEGEND-----GLASADSQFOSDEL 85
OY 53 PTQGIYETITDGYTVTKGVELVWGEKPRVYPPKPGDQKIYEIDPTLKDFRSHLDYRSEYR 112
DB 86 EYPDIEBETTCGA--GYADAQALNRVRVPPPSDQKIFQIDPMIGYKYHLEIRYSLR 143
OY 113 RIRAAIDQHEGGLBAFSGRYEKLGFTRSAEGITTYREMAPGANSALVGPNNMPPNADTM 172
DB 144 RIRSDIDEHGGLEAFSGRYEKFGRNRSAGITTYREMAPGANSALVGPNNMPPNADTM 203
OY 173 TRDDYGVWEFLPNNADGSPALPHGSRKIMDTPSGVDSI.SAMTKPSVQAPGELPENG 232
DB 204 SKNEFGWEFLPNNADGSPALPHGSRKIMDTPSGVDSI.PAMTKPSVQAPGELPENG 263
OY 223 IYVDPPEEKYVQHPQPKRRESLRIYESHIGMSPEPKINSYANRDEVLPRIKLGYN 292
DB 264 IYVDPPEEKYVQHPQPKRRESLRIYETHGMSPEPKINSYANRDEVLPRIKLGYN 323
OY 293 AVQIMAIQESHYYASFGYHTVNTFFAPSSRFGTPEDLKSLIDRAHELGLVLMIDIVSHSS 352
DB 324 AVQIMAIQESHYYASFGYHTVNTFFAPSSRFGTPEDLKSLIDRAHELGLVLMIDIVSHSS 383
OY 353 NNTLDGLNGDGDITDTHFHGPRGHHMMDSLLFYGSEVLR.FLLSNARWMLSEYFEDG 412
DB 384 NNTLDGLNGDGDITDTHFHGPRGHHMMDSLLFYGSEVLR.FLLSNARWMLSEYFEDG 443
OY 413 FRPDGVTSMNYTHHGLQWTFGNVGEYGFADVDVAVYVLMVNDLHGLHPDPAVSIGED 472
DB 444 FRPDGVTSMNYTHHGLQWTFGNVGEYGFADVDVAVYVLMVNDLHGLHPDPAVSIGED 503
OY 473 VSGMPFPCIPVDGSGVGFYRLHMAVADKMBLLKQSDSWKMGDIVHTVLTNNRMLEKCV 532
DB 504 VSGMPFPCIPVDGSGVGFYRLHMAVADKMBLLKQSDSWKMGDIVHTVLTNNRMLEKCV 563
OY 533 TYAESHDQALVGDKTIAFWLMDKMDYDPMALRPSIPR.LDRGLALHMTLVYMGLEGEG 592
DB 564 TYAESHDQALVGDKTIAFWLMDKMDYDPMALRPSIPR.LDRGLALHMTLVYMGLEGEG 623
OY 593 YLNPFGNGFGRPEKIDPRGPOTLPTGKVLPGNNNSYDKCRRRFPDGLADAF.LKXHQMEF 652
DB 624 YLNPFGNGFGRPEKIDPRGPOTLPTGKVLPGNNNSYDKCRRRFPDGLADAF.LKXHQMEF 683
OY 653 DQAMQHLEKKGFTSEHQYVSRKHEEDKVI.LFERGDLVFENPFHNSSEFDPYVSGSRP 712
DB 684 DQAMQHLEKKGFTSEHQYVSRKHEEDKVI.LFERGDLVFENPFHNSSEFDPYVSGSRP 743
OY 713 GKXKVALDSDDALFGGFSRLDHDVDYFTTEHPHDNPRPSVYTPPSTAYVYALTE 768
DB 744 GKXKVALDSDDALFGGFSRLDHDVDYFTTEHPHDNPRPSVYTPPSTAYVYALTE 799

RESULT 6
T06493
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) I - garden pea
N:Alternate names: starch branching enzyme I
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C:Accession: T06493

[illegible]

RESULT 7

1,4-alpha-glucan branching enzyme (EC 2.4.1.18) II - maize
N:Alternate names: starch branching enzyme II
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 18-Jun-1999

C:Accession: T02981
R:Fisher, D.K.; Boyer, C.D.; Hannah, L.C.

Plant Physiol. 102, 1045-1046, 1993
A:Title: Starch branching enzyme II from maize endosperm.

A:Reference number: 214808; MUID:94105320; PMID:8278524

A:Accession: T02981

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-799 <FIS>

A:Cross-references: EMBL:L08065; NID:g168482; PID:AAA18571.1; PID:g168483

A:Experimental source: cultivar W64Kx182E

C:Function:

A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-

A:Pathway: glycogen/starch biosynthesis

C:Superfamily: 1,4-alpha-glucan branching enzyme

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 80.2%; Score 3342; DB 2; Length 799;

Best Local Similarity 78.4%; Pred. No. 3e-243;

Matches 608; Conservative 67; Mismatches 79; Indels 22; Gaps 4;

4 FAVSAGTIGV-----ARPPAAQPEELQIPEDIEQTAENVMTGTAEKLESSE----- 52

35 FLTRGARVCGSTHGMRRAAAARAKAMVPEGEND-----GLASRADSAQFQDEL 85

53 PQQGIIVETITDVTAKVKKLVGEEKRVVPKPDGQKIYIDITLQDFRHLQDYREYR 112

86 EVDPISEETTCAG--GVADAQALNRVVRVPPSDGQKIFQIDPMLQGYKXKYLERYSLYR 143

113 RIRAAIDQHEGGLEAFSRGKELGFTRSABGITYREWAPAHSAALVGDNNMNPNDTM 172

144 RIRSDIDEHGGLEAFSRGKELGFTRSABGITYREWAPAHSAALVGDNNMNPNDTM 203

204 SKNEPQWVEIFLPNNADGTSPIPHGSRVKYKMDTPSGIKDISIPAMIKSYQAPGEIPLYDG 263

173 TRDDYQWVEIFLPNNADGSPALPHGSRVKYKMDTPSGVKSISAMIKSYQAPGEIPLYDG 232

223 IYDDPEEEKYVFOHQPKRPESLRITYESHTIGMSPEPKINSTANFDEVLPRIKLQYN 292

264 IYDDPEEEKYVFRHAQPKRPSKLRITYETHVGMSSPEPKINTYVNFDEVLPRIKLGYN 323

299 ANQIMAIQHSYASGYVNTNFAPSSRGTPEDEKSLIDRAHELGLVLMIDIVHSHS 352

324 AVQIMAIQHSYASGYVNTNFAPSSRGTPEDEKSLIDRAHELGLVLMIDIVHSHS 383

353 NNTLDGLNGFDGDTYHFGGPRGHMMWDSRLFNYSWEVLRLISNAEWLEEYKFDG 412

384 SNTLDGLNGFDGDTYHFGGPRGHMMWDSRLFNYSWEVLRLISNAEWLEEYKFDG 443

413 PFPDGTSMYTHGICOMFTTNGYGEFGATVDVAVYLMVNDLHGLHPDAVSGED 472

444 PFPDGTSMYTHGICOMFTTNGYGEFGATVDVAVYLMVNDLHGLYPEAVTTGED 503

473 VSGMPTFCIPVPDGGYGFDRILMAVADKWIILLKQSDSWRMGDIYHTLTNRWLEKCV 532

504 VSGMPTFCIPVPDGGYGFDRILMAVADKWIILLKQSDSWRMGDIYHTLTNRWLEKCV 563

533 TYAESHDQALVGDKTLAFWLMKDMYDPMALDRPSTPRIDRGALAHKIRLITVGLGEG 592

564 TYAESHDQALVGDKTLAFWLMKDMYDPMALDRPSTPRIDRGALAHKIRLITVGLGEG 623

593 YLNTMNGEERHPEWIDPPRGQTLPTGKVLPGNNNSVDKCRFRDLDADLARHGMQEF 652

624 YLNTMNGEERHPEWIDPPRGQTLPTGKVLPGNNNSVDKCRFRDLDADLARHGMQEF 683

RESULT 8

1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform SBE2.2 precursor - Arabidopsis
N:Alternate names: starch branching enzyme 2.2
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999

C:Accession: S65046
R:Fisher, D.K.; Gao, M.; Kim, K.N.; Boyer, C.D.; Gultinan, M.J.

Plant Mol. Biol. 30, 97-108, 1996

A:Title: Two closely related cDNAs encoding starch branching enzyme from Arabidopsis th

A:Reference number: S65045; MUID:96197401; PMID:8616246

A:Accession: S65046

A:Molecule type: mRNA

A:Residues: 1-800 <FIS>

A:Cross-references: EMBL:U22428; NID:g726489; PID:AA031100.1; PID:g726490

A:Note: only a part of the coding sequence is given

C:Genetics:

A:Genome: nuclear

C:Function:

A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-

A:Pathway: glycogen/starch biosynthesis

C:Superfamily: 1,4-alpha-glucan branching enzyme

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltr

F:1-40/Domain: transit peptide (chloroplast) #status predicted <TMP>

F:41-800/Product: 1,4-alpha-glucan branching enzyme isoform SBE2.2 #status predicted <Y

Query Match 78.1%; Score 3258; DB 2; Length 800;

Best Local Similarity 76.6%; Pred. No. 6.2e-237;

Matches 584; Conservative 75; Mismatches 32; Indels 32; Gaps 4;

18 AAQPEELQIE-----DIEQTEVAMTGTAEKLESSEPTQGIIVETITDG 64

54 AIASSEKLVVDNDDDPGSGQIFDLISQIY-----TAARTEDQTMV----- 100

65 VTKGYKELVGEKPRVVPKPDGQKIYEIDPTLKDFRSHLDYRSEYRRIRAAIDQHEGG 124

101 -----VKER--GVKRLIVPPDGGKIIYEIDPMLRTNNHLDVRYGQYKRLREIDYEGG 154

125 LEAFSGRYEKLGFTRSAIGITYREWAPAHSAALVGDNNMNPNDTTRDDYQWVEIFL 184

155 LEAFSGRYEKLGFTRSAIGITYREWAPAHSAALVGDNNMNPNDTTRDDYQWVEIFL 214

185 PNMADGSAIPHGSRVKLRMDTPSGVKSISAMIKSYQAPGEIIPNGIYDDPEEEKYV 244

215 PNMADGSAIPHGSRVKLRMDTPSGVKSISAMIKSYQAPGEIIPNGIYDDPEEEKYV 274

245 FOHPQPKPESLRITYESHTIGMSPEPKINSTANFDEVLPRIKLQYNVAVQIMAIQHSY 304

275 FKHPQPKPESLRITYESHTIGMSPEPKINSTANFDEVLPRIKLQYNVAVQIMAIQHSY 334

305 YASFGYHTNFFAPSSRGTPEDEKSLIDRAHELGLVLMIDIVHSHSNNNTLDGLNGFDG 364

335 YASFGYHTNFFAPSSRGTPEDEKSLIDRAHELGLVLMIDIVHSHSNNNTLDGLNGFDG 394

365 TDTHYFHGPRGHMMWDSRLFNYSWEVLRLISNAEWLEEYKFDGPRPDGVTSMYTT 424

395 TDTHYFHGPRGHMMWDSRLFNYSWEVLRLISNAEWLEEYKFDGPRPDGVTSMYTT 454

425 HHGLQMTFTGNGYGEFGATVDVAVYLMVNDLHGLHPDAVSGEDYSGMPTFCIPV 484

455 HHGLQMTFTGNGYGEFGATVDVAVYLMVNDLHGLHPDAVSGEDYSGMPTFCIPV 514

485 DGGVGFDRILMAVADKWIILLKQSDSWRMGDIYHTLTNRWLEKCVTYAESHDQALVG 544

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Db      515 DGVGVFDYRLHMAADKWIEMLKRDDEDMQGDIIYTLNRRWSEKISYAESHDQALVG 574
QY      545 DKTIAFWLMDKMDYFMAADLRPRIDRGIALHKKMRLVTMGIGSGGYLINFMGNEGHP 604
Db      575 DKTIAFWLMDKMDYFMAADLRPRIDRGIALHKKMRLVTMGIGSGGYLINFMGNEGHP 634
QY      605 EWIDPFRGPOTLPTGKVLPGNNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMHLEEKYG 664
Db      635 EWIDPFRGEBRLSDGSVIPGNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMHLEEKYG 694
QY      665 FMTSEHQVSRKHEEDKVIIFERGDIVFVFNFWMSNFPDYRGVCSPPGKYKVALDSDDA 724
Db      695 FMTSEHQVSRKHEEDKVIIFERGDIVFVFNFWMSNFPDYRGVCSPPGKYKVALDSDDP 754
QY      725 LFGGFSRLDHDVDYFTTEHPHNDPRSPFSVYTPSPRTAVYAL 766
Db      755 LFGGFSRLDHDVDYFTTEHPHNDPRSPFSVYTPSPRTAVYAL 796

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RESULT 9

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748392 1,4-alpha-glucan branching enzyme protein isoform SBE2.2 precursor - Arabidopsis thaliana
N:Alternate names: protein P17C15.70
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jun-2000
C:Accession: T48392
R:Bevan, M.; Pohl, T.; Weisenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24492
A:Accession: T48392
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-805 <BEV>
A:Cross-references: EMBL:AJ162506
A:Experimental source: cultivar Columbia; BAC clone P17C15
C:Genetics:
A:Map position: 5
A:Intons: 42/1: 81/3; 142/2; 175/2; 189/3; 209/3; 236/3; 275/3; 303/3; 344/2; 384/2; 42
A>Note: P17C15.70
C:Superfamily: 1,4-alpha-glucan branching enzyme

Query Match      78.1%; Score 3258; DB 2; Length 805;
Best Local Similarity 76.6%; Pred. No. 6.3e-237;
Matches 584; Conservative 75; Mismatches 71; Indels 32; Gaps 4;

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QY      18 AAAQPEELQIPE-----DIEBQTAENVMTGGTLEKLESSPTQGIYETTIDG 64
Db      59 AIGASEKVLVPDMLDDDPGSPQIFDLESQIMEY-----TEAVRTEDQIMNV----- 105
QY      65 VTGKVELVVGKPRVYKPGDQKIYEIDPTLKDFRSHLRYRSEYRIRAAIDQHEGG 124
Db      106 ----VVER--GVKPRIVPPRODGKTIYEIDPMLKTYNNHLDYRGQYKLAIEIDKYG 159
QY      125 LEAFSRGKELGFTSAEGITTYREMGAGASALVGFNNMNPADITMDYGYWEIFL 184
Db      160 LEAFSRGKELGFTSRDAGITTYREMGAGAKAASLIGDENMNNNSADITMRNFGWEIFL 219
QY      185 PNNADGSPALPHGRVYKIMDTBSGVKDSISAMIKFSVQAGEIPFNQIYDDPPEEKYV 244
Db      220 PNNYDGSPPALPHGRVYKIMDTBSGIXDSIPAMIKFSVQAGEIPFNQIYDDPPEEKYV 279
QY      245 FQHPQKRPSPSLRYESHIGMSPEPKINSYANFRDEVLPRIKLGYNAVOIMAQEESY 304
Db      280 FKHPQKRPSPSLRYEYHVGMSSTBPWNTYANFRDVLPRIKLGYNAVOIMAQEESY 339
QY      305 YASFGYVNTFPFAPSSRFQPEDIKSLIDRAHEIGLVLMIDIVSHSSNNLTDLGNGFDG 364
Db      340 YASFGYVNTFPFAPSSRCGTPEELKSLIDRAHEIGLVLMIDIVSHASKNTLDGLNMGFDG 399
QY      365 TDTHYFPGGRGHMMWDSRLFNYSWEVLRFLLSNAWMLLEYKFDPRPDGUTSMYIT 424
Db      400 TDTHYFPGGRGHMMWDSRLFNYSWEVLRFLLSNAWMLLEYKFDPRPDGUTSMYIT 459

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QY      425 HHGQMTPTNGYGEYFEGATVDVAVYVLMVNDLHGHLPAVSGEDVSGMFTFCIPVP 484
Db      460 HHGQSVGTGYTEYFEGLETDVDAVNYVLMVNDMLHGLYPAITVGEDVSGMFTFCIPVQ 519
QY      485 DGVGVFDYRLHMAADKWIEMLKRDDEDMQGDIIYTLNRRWSEKISYAESHDQALVG 544
Db      520 DGVGVFDYRLHMAADKWIEMLKRDDEDMQGDIIYTLNRRWSEKISYAESHDQALVG 579
QY      545 DKTIAFWLMDKMDYFMAADLRPRIDRGIALHKKMRLVTMGIGSGGYLINFMGNEGHP 604
Db      580 DKTIAFWLMDKMDYFMAADLRPRIDRGIALHKKMRLVTMGIGSGGYLINFMGNEGHP 639
QY      605 EWIDPFRGPOTLPTGKVLPGNNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMHLEEKYG 664
Db      640 EWIDPFRGEBRLSDGSVIPGNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMHLEEKYG 699
QY      665 FMTSEHQVSRKHEEDKVIIFERGDIVFVFNFWMSNFPDYRGVCSPPGKYKVALDSDDA 724
Db      700 FMTSEHQVSRKHEEDKVIIFERGDIVFVFNFWMSNFPDYRGVCSPPGKYKVALDSDDP 759
QY      725 LFGGFSRLDHDVDYFTTEHPHNDPRSPFSVYTPSPRTAVYAL 766
Db      760 LFGGFSRLDHDVDYFTTEHPHNDPRSPFSVYTPSPRTAVYAL 801

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RESULT 10

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707743 probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform II - potato (fragment)
N:Alternate names: starch branching enzyme II
C:Species: Solanum tuberosum (potato)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07743
R:Larsson, C.T.; Khoshnoodi, J.; Ek, B.; Raek, L.; Larsson, H.
Plant Mol. Biol. 37, 505-511, 1998
A:Title: Molecular cloning and characterization of starch-branching enzyme II from pot;
A:Reference number: Z16110; MUID:98278379; PMID:96117817
A:Accession: T07743
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <LAR>
A:Cross-references: EMBL:AJ000004; NID:92764395; PID:CA03846.1; PID:92764396
A:Experimental source: cv. Amanda
A:Gene: Sbe-II
C:Function:
A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-
A:Pathway: glycogen/starch biosynthesis
C:Superfamily: 1,4-alpha-glucan branching enzyme
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match      76.9%; Score 3207; DB 2; Length 830;
Best Local Similarity 72.7%; Pred. No. 4.6e-233;
Matches 587; Conservative 83; Mismatches 89; Indels 48; Gaps 6;

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QY      2 ATPAVSGATL--GVARPPAAQPEELQIPE-----DIEBQTAENVMTGGTLEKLESSPTQGIYETTIDG 37
Db      12 STVAASGKVLVPGTQSDSSSTGQEFETBSPNSPASTDVDSSTVHAASQITENDDV 71
QY      38 ---VNMGTGTAL-----KLESSEPTQGIYETTIDGVTGKVELVGEKPRVY 81
Db      72 EPSSDLVGSVEELDPASSIQLOEGGKLESKTLNTEETIIDSQR--IRE-----RGI 123
QY      82 PKPGDQKTIYEIDPTLKDRSHLDYRSEYRIRAAIDQHEGGLEAFSRGKELGFTRSA 141
Db      124 PPGGIGQKIYEIDPLTNRQHLDYISQYKTLREAIIDKXEGGLEAFSRGKELGFTRSA 183
QY      142 EGITTYREMGAGASALVDFNNMNPADITMDYGYWEIFL PNNADGSPALPHGRVYK 201
Db      184 TGITTYREMGAGASALIDFPNNWMDANADITMRNFGWEIFL PNNYDGSPPALPHGRVYK 243
QY      202 TMDPDSGYKDSISAMIKFSVQAGEIPFNQIYDDPPEEKYV FQHPQKRPSPSLRYES 261

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Db 244 IRMDTSGVSDSIPTAMINYSQJLDELFPNGIYYDPPEEERYIFQHPKPKSLRIYES 303
 Qy 262 HIGMSSPEPKINSYANFRDEVLPRIKELGYNVAOIMAIQEHSYIASFGYHTNFPAPSSR 321
 Db 304 HIGMSSPEPKINSYANFRDEVLPRIKELGYNVAOIMAIQEHSYIASFGYHTNFPAPSSR 363
 Qy 322 FGRPEDLKSLIDRAHEGLVLMIDIVSHSNNLTDLNGSPDPTDTHFHGPPGHMMW 381
 Db 364 FGRPEDLKSLIDRAHEGLVLMIDIVSHSNNLTDLNGSPDPTDTHFHGPPGHMMW 423
 Qy 382 DSELPYVGSWEVLRFLISNARMWLEEKFPDGFREDGYTSMYTHHGLQMTFTGNVGEYFG 441
 Db 424 DSELPYVGSWEVLRFLISNARMWLEEKFPDGFREDGYTSMYTHHGLQMTFTGNVGEYFG 483
 Qy 442 FATDVDAVYVLMVNDLIHGLHPDVAISIGEDVSGMPTFCIPVDGSGVFDYRLHVAADK 501
 Db 484 LATDVDAVYVLMVNDLIHGLHPDVAISIGEDVSGMPTFCIPVDGSGVFDYRLHVAADK 543
 Qy 502 WTELLKQSDBSWKMGGDIVHTLTNRRLMEKCVTAESHDQALVGDKTAFWLMDKMDYFM 561
 Db 544 WTELLKQSDBSWKMGGDIVHTLTNRRLMEKCVTAESHDQALVGDKTAFWLMDKMDYFM 603
 Qy 562 ALDRPSTPRIDRGIALHKMRLVTMGLGEGYLNFMGNEFGHPMIDFPFRGPQTLPTGKY 621
 Db 604 ALDRPSTPRIDRGIALHKMRLVTMGLGEGYLNFMGNEFGHPMIDFPFRGPQTLPTGKY 663
 Qy 622 LPGNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEKYGEMTSEHQYVSRKHEDKV 681
 Db 664 LPGNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEKYGEMTSEHQYVSRKHEDKV 723
 Qy 682 VIFERGDLVFNFMNSNFEDYRVGCSRPGRKXVALDSDDALFGFSRLDHDVDYTTT 741
 Db 724 VIFERGDLVFNFMNSNFEDYRVGCSRPGRKXVALDSDDALFGFSRLDHDVDYTTT 783
 Qy 742 BHPDNRPRSFSVYTPSRATVAVYALTE 768
 Db 784 BHPDNRPRSFSVYTPSRATVAVYALTE 810

RESULT 11

starch branching enzyme II (imported) - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
 C:Accession: B84780
 R:Linn, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;
 Ems, D.; Niernann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; WUID:20083487; PMID:10617197
 A:Accession: B84780
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-858 <STO>
 A:Cross-references: GB:AE002093; NID:g4561160; PIDN:AAD24644.1; GSPDB:GN00139
 A:Gene: At2g36390
 A:Map position: 2
 C:Superfamily: 1,4-alpha-glucan branching enzyme

Query Match 75.7%; Score 3155; DB 2; Length 858;
 Best Local Similarity 75.2%; Pred. No. 4e-229;
 Matches 561; Conservative 90; Mismatches 79; Indels 16; Gaps 3;

Qy 23 EELQIPEDIEQTAENMTGTAEKLESSPTQGIYVITMDGVTKGVKELVGEKPRVP 82
 Db 109 EEAQETETL-DQTSALSTSGSISYKEDFAKMSHV-----DQEVGQ-RKIP 152
 Qy 83 KPGDGGKIVIEDTLKDFRSHLDYRSEYVRIRAPADIDQHEGGLAFAFGYKGLGFTSAAE 142
 Db 153 PGDGGKIVIEDTLKDFRSHLDYRSEYVRIRAPADIDQHEGGLAFAFGYKGLGFTSAAE 212

Qy 143 GITYREKAPGASALVGDENNMMNPADMTNDYGVWEIPLNNMADGSPALPHGSRVKI 202
 Db 213 GITYREKAPGASALVGDENNMMNPADMTNDYGVWEIPLNNMADGSPALPHGSRVKI 272
 Qy 203 RMDTSGVSDSIAMIKFVQAPGEIPFNGIYYDPPEEERYIFQHPKPKSLRIYESH 262
 Db 273 RMDTSGVSDSIAMIKFVQAPGEIPFNGIYYDPPEEERYIFQHPKPKSLRIYESH 332
 Qy 263 IGMSSPEPKINSYANFRDEVLPRIKELGYNVAOIMAIQEHSYIASFGYHTNFPAPSSR 322
 Db 333 IGMSSPEPKINSYANFRDEVLPRIKELGYNVAOIMAIQEHSYIASFGYHTNFPAPSSR 392
 Qy 323 GTPEDLKSLIDRAHEGLVLMIDIVSHSNNLTDLNGSPDPTDTHFHGPPGHMMW 382
 Db 393 GTPEDLKSLIDRAHEGLVLMIDIVSHSNNLTDLNGSPDPTDTHFHGPPGHMMW 452
 Qy 383 SELPYVGSWEVLRFLISNARMWLEEKFPDGFREDGYTSMYTHHGLQMTFTGNVGEYFG 442
 Db 453 SELPYVGSWEVLRFLISNARMWLEEKFPDGFREDGYTSMYTHHGLQMTFTGNVGEYFG 512
 Qy 443 ATDVDAVYVLMVNDLIHGLHPDVAISIGEDVSGMPTFCIPVDGSGVFDYRLHVAADK 502
 Db 513 ATDVDAVYVLMVNDLIHGLHPDVAISIGEDVSGMPTFCIPVDGSGVFDYRLHVAADK 572
 Qy 503 TELLKQSDBSWKMGGDIVHTLTNRRLMEKCVTAESHDQALVGDKTAFWLMDKMDYFM 562
 Db 573 TELLKQSDBSWKMGGDIVHTLTNRRLMEKCVTAESHDQALVGDKTAFWLMDKMDYFM 632
 Qy 563 LDRPSTPRIDRGIALHKMRLVTMGLGEGYLNFMGNEFGHPMIDFPFRGPQTLPTGKY 622
 Db 633 LDRPSTPRIDRGIALHKMRLVTMGLGEGYLNFMGNEFGHPMIDFPFRGPQTLPTGKY 692
 Qy 622 LPGNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEKYGEMTSEHQYVSRKHEDKV 682
 Db 692 LPGNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEKYGEMTSEHQYVSRKHEDKV 752
 Qy 682 VIFERGDLVFNFMNSNFEDYRVGCSRPGRKXVALDSDDALFGFSRLDHDVDYTTT 742
 Db 753 VIFERGDLVFNFMNSNFEDYRVGCSRPGRKXVALDSDDALFGFSRLDHDVDYTTT 812
 Qy 742 BHPDNRPRSFSVYTPSRATVAVYALTE 768
 Db 812 BHPDNRPRSFSVYTPSRATVAVYALTE 838

RESULT 12

865045
 1,4-alpha-glucan branching enzyme (BC 2.4.1.18) isoform SBE2.1 precursor - Arabidopsis
 N:Alternate names: starch branching enzyme 2.1
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999
 C:Accession: S65045
 R:Fisher, D.K.; Gao, M.; Kim, K.N.; Boyer, C.D.; Guiltinan, M.J.
 Plant Mol. Biol. 30, 97-108, 1996
 A:Title: Two closely related cDNAs encoding starch branching enzyme from Arabidopsis th
 A:Reference number: S65045; WUID:196197401; PMID:8616246
 A:Molecule type: mRNA
 A:Residues: 1-854 <FIS>
 A:Cross-references: EXBL:U18817; NID:g619938; PIDN:AAB03099.1; PID:g619939
 A>Note: only a part of the coding sequence is given

C:Genetics: nuclear

A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-
 A:Pathway: glycogen/starch biosynthesis
 A>Note: final step in biosynthesis of glycogen or amylopectin
 C:Superfamily: 1,4-alpha-glucan branching enzyme
 C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltran
 F:1-47/Domain: transil peptide (chloroplast) #status predicted <TNP>
 F:48-854/Product: 1,4-alpha-glucan branching enzyme isoform SBE2.1 #status predicted <M

Best Local Similarity 74.8%; Pred. No. 1.3e-227;
Matches 558; Conservative 91; Mismatches 81; Indels 16; Gaps 3;

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QY 23 EEQIPEDIEQAEVMTGTAKLSSSEPTQGITITDGVTKGVYELVGEKPRVP 82
Db 105 EEAQETITL-DQTSALSTSGSISKEDPAKSHSV-----DQEVGQ--RKIP 148
QY 83 KPQDQKIVEIDPTLKDPRSHLDYRSEYRRIRAAIDQHBGGLFAFSNGYEKLGFTRSAE 142
Db 149 PPDDQKRIYIDPELNSHRNHLDYRGGYRKLREIDNKGGLFAFSNGYEKLGFTRSAT 208
QY 143 GTTYREAPAGASALVGDFFNNMPPNADTYTRDYGVEILPNNADSPALPHSRKXI 202
Db 209 GITYREAPAGAKASLIGDFNNMNAKSDVMAANDFGVEILPNNADSPALPHSRKXI 268
QY 203 RMDTPSGVKSISAMIKFSVQAPGEIPNGIYYDPPEEKYVFPQPKRPESLRIYESH 262
Db 269 RMDTPSGIKSIPAMIKFSVQAPGEIPNGIYYDPPEEKYVFPQPKRPESLRIYESH 328
QY 263 IGNSPEPKINSYANFDEVLPRIKLGYNAVQIMAIQESHVYASFGYHVTNFEAPSSRF 322
Db 329 VGNSTPEKINTYANFRDVLPRIKLGYNAVQIMAIQEHAYVYASFGYHVTNFEAPSSRF 388
QY 323 GTPEBDKSLIDRAELGLVMDIVHSHSNNTLDGLNGFQGTDTYHFGGRGHHMMMD 382
Db 389 GTPEBDKSLIDRAELGLVMDIVHSHSNNTLDGLNGFQGTDTYHFGGRGHHMMMD 448
QY 383 SRLFNYSWEVLRFLISARWMLSEYKDFPFDGVTSMYTHGLQMTFTNGSEYEGF 442
Db 449 TRLENYSWEVLRFLISARWMLSEYKDFPFDGVTSMYTHGLQMTFTNGSEYEGF 508
QY 443 ATVDVAVVYMLVNDLHGLHPDAVSIQEDVSGMPTFCIPVBDGVDGYRLHMAVADKW 502
Db 509 STDVDAVYVYMLVNDLHGLHPDAVSIQEDVSGMPTFCIPVBDGVDGYRLHMAVADKW 568
QY 503 TELIKQSDSKMGDLYHTLTNRRLKCYTYAESHDQALVGDXTIAFLMDKMDYDEKA 562
Db 569 TELIKQSDSKMGDLYHTLTNRRLKCYTYAESHDQALVGDXTIAFLMDKMDYDEKA 628
QY 563 LDRPSTRIDGIALHKMIRLYVTMGLGEGYINFMNGEPHEMIDPPRPOTLPTGKYL 622
Db 629 VDRQATPRVDGIALHKMIRLYVTMGLGEGYINFMNGEPHEMIDPPRPOTLPTGKYL 688
QY 623 PGNNSYDKCRRRPDLGADFLRYHGMQEFDAQMHLEEKYFMTSEHOYVRKHEEDKY 682
Db 689 AGNNGSYKSRRRPDLGADFLRYHGMQEFDAQMHLEEKYFMTSEHOYVRKHEEDKY 748
QY 683 IIFERGDVYVFNPFMWSNPFYRGGCSFGKAKYALDSDDLFGGFSRLDHDVYFTRE 742
Db 749 IIFERGDVYVFNPFMWSNPFYRGGCSFGKAKYALDSDDLFGGFSRLDHDVYFTRE 808
QY 743 HPDNRPSFSYVTPSRATVAVYALTE 768
Db 809 GRHDDRPFCSFMYVAFCRTAIVYVAAVD 834

```

RESULT 13

T06578
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbel precursor - wheat
N/Alternate names: starch branching enzyme I
C/Species: Triticum aestivum (common wheat)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #ext_change 20-Jun-2000
C/Accession: T06578
R:Chibbar, R.N.
submitted to the EMBL Data Library, April 1997
A/Reference number: Z15772
A/Accession: T06578
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-830 <CH1>
A/Cross-references: EMBL:Y12320; PION:CAA72987.1
A/Experimental source: cv. Fielder; kernels at 12 days post-anthesis
C/Genetics:

A/Gene: Sbel
C/Function:
A/Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-
A/pathway: glycogen/starch biosynthesis
C/Superfamily: 1,4-alpha-glucan branching enzyme
C/Keywords: amyloplasi; glycogen/starch biosynthesis; glycosyltransferase; hexosyltran-
F.1-61/Domains: transit peptide (amyloplasi) #status predicted <TMP>
F.62-830/Product: 1,4-alpha-glucan branching enzyme sbel #status predicted <MAT>

Query Match 52.6%; Score 2193.5; DB 2; Length 830;
Best Local Similarity 55.7%; Pred. No. 9.4e-157;
Matches 408; Conservative 104; Mismatches 174; Indels 47; Gaps 9;

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QY 51 SEPTQGITITDGVTKGVYELVGEKPRVPKPGQKQKYEIDPTLKDPRSHLDYRSE 110
Db 63 SAPRDYVYATADG-----VGDLF-----IYDDPKFAGKEHFSYMKK 102
QY 111 YRIRAPAIQHBGGLFAFSNGYEKLGFTSAEGITYREMAPAGASALVGDFFNNMPPNAD 170
Db 103 YDDQKSIKHBGGLFAFSNGYEKLGFTSAEGITYREMAPAGASALVGDFFNNMPPNAD 162
QY 171 TWTRDYGVEILPNNADSPALPHSRKXIMDTPSGY-KDSISAMIKFSVQAPGEI- 228
Db 163 RMTKMDYGVWSIRI-SHVNGKPAIPHNSKYKFFHRGDLVMDVRVPMIRVATPDASFG 221
QY 229 -PENGYYDPPEEKYVFPQPKRPESLRIYESHIGNSPEPKINSYANFRDEVLPRIK 287
Db 222 APDGVHMDPPSGERYVFPQPKRPESLRIYESHIGNSPEPKINSYANFRDEVLPRIK 281
QY 288 RLGYNVQIMAIQESHVYASFGYHVTNFEAPSSRFGTPEBDKSLIDRAELGLVMDIV 347
Db 282 ANNTYVQIMAIQESHVYASFGYHVTNFEAPSSRFGTPEBDKSLIDRAELGLVMDIV 341
QY 348 HSHSNNTLDGLNGFP--GTDTHYHGGPRGHHMMDSRLFNYSWEVLRFLISNAW 404
Db 342 HSHSNNTLDGLNGFP--GTDTHYHGGPRGHHMMDSRLFNYSWEVLRFLISNAW 401
QY 405 LBEYKDFPFDGVTSMYTHGLQMTFTNGYEGFATPTVDVAVYVYMLVNDLHGLAP 464
Db 402 MBEFMEGDFPFDGVTSMYTHGLQMTFTNGYEGFATPTVDVAVYVYMLVNDLHGLAP 461
QY 465 DAVISIEDVSGMPTFCIPVBDGVDGYRLHMAVADKWIELKQSD-SWQAGDIVHTLT 523
Db 462 EATVVAEDVSGMPTFCIPVBDGVDGYRLHMAVADKWIELKQSD-SWQAGDIVHTLT 521
QY 524 NREMLEKCYTYAESHDQALVGDXTIAFLMDKMDYDEMALDREPTPRIDGIALHKMIRL 583
Db 522 NREMLEKCYTYAESHDQALVGDXTIAFLMDKMDYDEMALDREPTPRIDGIALHKMIRL 581
QY 584 VTMGLGEGYINFMNGEPHEMIDPPRPOTLPTGKYLPGNNSYDKCRRRPDLGADAF 643
Db 582 ITMALGGDGYINFMNGEPHEMIDPPRPOTLPTGKYLPGNNSYDKCRRRPDLGADAF 640
QY 644 LRYHGMQEFDAQMHLEEKYFMTSEHOYVRKHEEDKYIIFERGDVYVFNFMWSNPF 703
Db 631 LRYHGMQEFDAQMHLEEKYFMTSEHOYVRKHEEDKYIIFERGDVYVFNFMWSNPF 690
QY 704 DYRVCGRPGKRYKALDSDDLFGGFSRLDHDVYFTT-----EHPDNRPSFSY 755
Db 691 GYKYGCDLPGKYKALDSDLMFGGHSRVAHDNDHFTSPBGVPGVETNFNRPNSFKIL 750
QY 756 TPSTATVAVYALTE 768
Db 751 SPSTCVAYTRVE 763

```

RESULT 14

T07824
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) I (clone sbel7) - potato (fragment)
C/Species: Solanum tuberosum (potato)
C/Date: 14-May-1999 #sequence_revision 14-May-1999 #ext_change 21-Jul-2000
C/Accession: T07824
R:Koshinoki, J.; Blomqvist, A.; Ek, B.; Raek, L.; Larsson, H.

Tue Apr 20 10:02:30 2004

us-09-508-377-12.rpr

Page 10

Db 432 YFSLDTVDVAIVYWMANHLHKLLEFATVAEDVSGMPVLCRPVDEG3GVGDFPRLAMAI 491
QY 499 ADKXIEJLK-QSDESKKGGDIYHTLTNRRLKCYTVAESHQALVGDKTIAFWLMDKM 557
Db 492 PDRWIDYLNKEDRKSMSSEIVQTLNRRYTEKCIAYASHDQIVGDKTIAFLMDKEM 551
QY 558 YDFVALDRPSTPRIDRGIALHQMIRLVTMGLGEGYLNFMGNEFGHPENIDFPFGPQTLP 617
Db 552 YTGMSDLOPASPTINRGIALQKMHFTMALGGDGYLNFMGNEFGHPENIDFP 605
QY 618 TGKVLPGNNNSYDKCRRRFDLGADFLRYHGMQEPDQAMOHLEEKYGFNTSHQYVSRKA 677
Db 606 -----EGNWSGYDKCRQMSLVTDHLRYKYNNAFDQAMNALLEEFSFLSSKQIVSDMN 660
QY 678 EEDKVIIPERGDVVFNFHMSNFFDYRVGGRPGKYKVALSDDALFGFSRLDHDVD 737
Db 661 EKDKVIVFERGDLVVFNFHFNKTYKGXKVGCDLPGKIRVALSDALVFGHGRVGHADV 720
QY 738 YFTT-----EHPDNRPRSFSVYTPSRITAVY 764
Db 721 HFTSBEGMPSVETFNFNRRPNSFKVLSPPRTCVAY 755

Search completed: April 15, 2004, 08:38:41
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2004, 08:35:15 / Search time 18 Seconds
(without alignments)

2221.660 Million cell updates/sec

Title: US-09-508-377-12

Perfect score: 4169
Sequence: 1 MATFVSGATLGVARRPAAA.....PRFSVYTPSRVAVYALTE 768

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3342	80.2	799	1	GLGB_MAIZE
2	2166.5	52.0	820	1	GLGB_ORISA
3	2140	51.3	702	1	GLGB_HUMAN
4	2122.5	50.9	861	1	GLGB_SOLTU
5	1795.5	43.1	704	1	GLGB_YEAST
6	628	15.1	715	1	GLGB_VIBVU
7	624	15.0	773	1	GLGB_SYNP7
8	620	14.9	755	1	GLGB_VIBPA
9	592.5	14.2	666	1	GLGB_VIBCH
10	579	13.9	734	1	GLGB_NITRU
11	576	13.8	762	1	GLGB_NITRU
12	574	13.8	737	1	GLGB_PHTIO
13	573	13.7	770	1	GLGB_SYNP3
14	571.5	13.7	637	1	GLGB_OCEIH
15	568.5	13.6	731	1	GLGB_COREF
16	568	13.6	766	1	GLGB_SYNEL
17	564.5	13.5	741	1	GLGB_CORGL
18	562	13.5	751	1	GLGB_ANMSP
19	558	13.4	730	1	GLGB_HAINT
20	557	13.4	730	1	GLGB_PASMU
21	555.5	13.3	734	1	GLGB_AGRU
22	554	13.3	727	1	GLGB_YERPE
23	553.5	13.3	728	1	GLGB_ECOLI
24	552.5	13.3	728	1	GLGB_SHIFL
25	550.5	13.2	728	1	GLGB_DEIRA
26	550.5	13.2	728	1	GLGB_ECO57
27	549.5	13.2	630	1	GLGB_AQUAE
28	548.5	13.2	728	1	GLGB_ECOL6
29	548.5	13.2	728	1	GLGB_SALTI
30	548.5	13.2	728	1	GLGB_SALTI
31	548	13.1	725	1	GLGB_AGRU5
32	544.5	13.1	721	1	GLGB_BRAVA
33	541.5	13.0	621	1	GLGB_RHOMR

34	540.5	13.0	634	1	GLGB_LACGL	O890j1 lactobacill
35	540.5	13.0	666	1	GLGB_BACGL	P30537 bacillus ca
36	540	13.0	639	1	GLGB_BACST	P30538 bacillus st
37	538.5	12.9	724	1	GLB1_XANAC	Q8p13 xanthomonas
38	537	12.9	732	1	GLGB_PSEAR	Q91w2 pseudomonas
39	535.5	12.8	731	1	GLGB_MYCBO	P59816 mycobacteri
40	530.5	12.7	664	1	GLB2_GLOBE	O8xx15 clostridium
41	530	12.7	731	1	GLGB_ERWCH	O895c5 erwina chr
42	525.5	12.6	731	1	GLGB_MYCTU	Q10625 mycobacteri
43	525.5	12.5	724	1	GLB1_XANCP	Q8pe48 xanthomonas
44	521	12.5	639	1	GLGB_BUTFI	P30539 butyrivibri
45	520	12.5	737	1	GLGB_BIFLO	Q89510 bifidobacte

ALIGNMENTS

RESULT 1
GLGB_MAIZE STANDARD; PRT; 799 AA.
ID GLGB_MAIZE
AC Q08047;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1,4-alpha-glucan branching enzyme IIB, chloroplast precursor
DE (EC 2.4.1.18) (Starch branching enzyme IIB) (O-enzyme).
GN SBE1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 58-65.
RC STRAIN=cv. M64A X 182E; TISSUE=Endosperm;
RX MEDLINE=94105320; PubMed=8278524;
RA Fisher D.K., Boyer C.D., Hannah L.C.;
RT "Search branching enzyme II from maize endosperm.";
RL Plant Physiol. 102:1045-1046(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 248-271 AND 305-315.
RC STRAIN=cv. B73; TISSUE=Endosperm;
RX MEDLINE=95152344; PubMed=7849565;
RA Guan H.P., Baba T., Preiss U.;
RT "Expression of branching enzyme II of maize endosperm in Escherichia coli.";
RL Cell. Mol. Biol. 40:981-986(1994).
CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic linkages in glycogen by scission of a 1,4-alpha-linked oligosaccharide from growing alpha-1,4-glucan chains and the subsequent attachment of the oligosaccharide to the alpha-1,6 position.
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of starch.
CC -1- PATHWAY: Starch biosynthesis; third step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast; Amyloplast.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb.ch/announce/> or send an email to license@isb-sib.ch).
CC EMBL; L08065; AAA18571.1; -
CC PIR; T02981; T02981.
CC MaledDB; 63943; -
CC InterPro; IPR006047; Alpha_amy1_cat.
CC InterPro; IPR004193; Glyco_hydro_13N.
CC Pfam; PF00128; alpha-amy1ase; 1.

DR Pfam: PF02922; isoamylase N; 1.
 KW Glycogen biosynthesis; Starch biosynthesis; Transferase;
 KM Glycosyltransferase; Amyloplast; Chloroplast; Transit peptide.
 FT TRANSIT 1 57 CHLOROPLAST (AMYLOPLAST).
 FT CHAIN 58 799 1,4-ALPHA-GLUCAN BRANCHING ENZYME 11B.
 FT ACT_SITE 341 341 BY SIMILARITY.
 FT ACT_SITE 376 376 BY SIMILARITY.
 FT ACT_SITE 381 381 BY SIMILARITY.
 FT ACT_SITE 445 445 BY SIMILARITY.
 FT ACT_SITE 447 447 BY SIMILARITY.
 FT ACT_SITE 502 502 BY SIMILARITY.
 FT ACT_SITE 569 569 BY SIMILARITY.
 FT ACT_SITE 570 570 BY SIMILARITY.
 SQ SEQUENCE 799 AA; 90517 MW; 0B440E0377B8087A C6C64;

Query Match 80.2%; Score 3342; DB 1; Length 799;

Best Local Similarity 78.4%; Pred. No. 3,1e-239;
 Matches 608; Conservative 67; Mismatches 79; Indels 22; Gaps 4;

4 PAVSGATLV----APPAAQPEELQIPEDIEQTAENVMTGTAKLESSF----- 52
 35 FLTRGARVCGSGTHGARRAAAKAAVAVPGEEND-----GLARADSAQSDSL 85
 53 PFGIVETITDGVKVKELVVGKPRVVPKPGDGOKIYEIDPTLCKDRSHLDYRSEYR 112
 86 EVDISEETGGA--GVAQAALNRVAVPPSPDQKIFQIDPMIQKIHLEYRSLYR 143
 113 RIRAIIDQHEGGLAEFGRGYEKLFTSAGEITYREMAPGAASALVQDFNNMNNADTM 172
 144 RIRSDIDHEGGLAEFGRGYEKLFTSAGEITYREMAPGAASALVQDFNNMNNADTM 203
 173 TRDDYGVWEIPLPNNADGSPAIPIHOSRYKINMDTPSGYKDSISATIKSVQAPGPIPN 232
 204 SKNEFGWEIPLPNNADGSPAIPIHOSRYKINMDTPSGYKDSISATIKSVQAPGPIPN 263
 233 IYVDPREEKVPQHPQKRESIRIYESHIGMSPEPKINSYAFREBVLPRIKRLGN 292
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 293 AVQIMAIQEHSSYASFGYHVTNFFAPSSRFPTEDLKSLIDRAHELGLVMDIVSHSS 352
 324 AVQIMAIQEHSSYASFGYHVTNFFAPSSRFPTEDLKSLIDRAHELGLVMDIVSHSS 383
 353 NNTLDGLNGFGDTTHYHGGRRGHMWDRLFNYSMEVLRFLLSNARWMLSEYKPRG 412
 384 NNTLDGLNGFGDTTHYHGGRRGHMWDRLFNYSMEVLRFLLSNARWMLSEYKPRG 443
 413 FRFGVTSMTYTHGLQMTFTGNVGEFGFATDPAVVYLMVNDLHGLHDAVSGID 472
 444 FRFGVTSMTYTHGLQMTFTGNVGEFGFATDPAVVYLMVNDLHGLHDAVSGID 503
 473 VSGMPTFCIPVDPGVGFDFYRLHMAVADKMIELKQSDSAPKMGDIVHTLNNRMLEKY 532
 504 VSGMPTFCIPVDPGVGFDFYRLHMAVADKMIELKQSDSAPKMGDIVHTLNNRMLEKY 563
 533 TYAASHDQALVGDKTIATWMDKMDYDFALALRPSTPRIDRGIALHKMRLVTMGIGGSG 592
 564 TYAASHDQALVGDKTIATWMDKMDYDFALALRPSTPRIDRGIALHKMRLVTMGIGGSG 623
 593 YLNFNGNFGHEMIDFPRGPOTLPTGKVLPGNNNSYDKCRSRFDLGDADFLRYHQMOEF 652
 624 YLNFNGNFGHEMIDFPRGPOTLPTGKVLPGNNNSYDKCRSRFDLGDADFLRYHQMOEF 683
 653 DOAMQHELEKYGMTSEHQYVSRKHEEDKVIIFERGDLVFNFNHNSFPDYRVGCSR 712
 684 DOAMQHELEKYGMTSEHQYVSRKHEEDKVIIFERGDLVFNFNHNSFPDYRVGCSR 743
 713 GKIKYALSDDDLFGGFSRLDHDVYFTTEHHNDNPRFSVYTPRTAVVYALTE 768
 744 GYKRVVLDSADGLFGGFSRIHHAHEFTADCSHNDPRFSVYTPRTAVVYALTE 799

GLGB_ORYSA
 ID ID GLGB_ORYSA STANDARD: PRT; 820 AA.
 AC 001001-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Starch branching enzyme) (Q-enzyme).
 DE SBE1.
 GN Oryza sativa (Rice).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocaulaceae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Japonica, TISUR-Endosperm;
 RA Nakamura Y., Yamamoto H.;
 RT "Nucleotide sequence of a cDNA encoding starch-branching enzyme, or O-enzyme I, from rice endosperm."
 RL Plant Physiol. 99:1265-1266(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93204882; PubMed=8455548;
 RA Kawasaki T., Mizuno K., Baba T., Shimada H.;
 RT "Molecular analysis of the gene encoding a rice starch branching enzyme."
 RL Mol. Gen. Genet. 237:10-16(1993).
 RL 1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic linkages in glycogen by scission of a 1,4-alpha-linked oligosaccharide from growing alpha-1,4-glucan chains and the subsequent attachment of the oligosaccharide to the alpha-1,6 position.
 CC 1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of starch.
 CC 1- PATHWAY: Starch biosynthesis; third step.
 CC 1- SUBUNIT: Monomer.
 CC 1- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
 CC 1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 CC EMBL: D10752; BAA01584.1; --
 CC EMBL: D10838; BAA01616.1; --
 DR Gramene; 001401; --
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR004193; Glyco_hydro_13n.
 DR Pfam; PF00128; alpha-amylose; 1.
 DR Pfam; PF02922; isoamylase N; 1.
 KM Starch biosynthesis; Transferase; Glycosyltransferase; Amyloplast; Chloroplast.
 FT MOD_RES 1 1 BLOCKED.
 FT ACT_SITE 300 300 BY SIMILARITY.
 FT ACT_SITE 335 335 BY SIMILARITY.
 FT ACT_SITE 340 340 BY SIMILARITY.
 FT ACT_SITE 407 407 BY SIMILARITY.
 FT ACT_SITE 409 409 BY SIMILARITY.
 FT ACT_SITE 464 464 BY SIMILARITY.
 FT ACT_SITE 533 533 BY SIMILARITY.
 FT ACT_SITE 533 533 BY SIMILARITY.
 FT CONFLICT 13 13 P -> A (IN REF. 2).
 FT CONFLICT 715 753 VGHVDHFTSDEGMPVEITNNRPNNSFKULSPRTCV -> LAMMWITSLRPRECEYKQISTALTLSKSPRPV
 SQ SEQUENCE 820 AA; 93262 MW; A687CF9396F59DF C6C64;

Query Match 52.0%; Score 2166.5; DB 1; Length 820;
 Best Local Similarity 57.8%; Pred. No. 2.9e-152;

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Matches 402; Conservative 104; Mismatches 160; Indels 29; Gaps 10;
Oy 86 DQGIYEIDPTLKDRSHLDYRSEYRIRAAIDHGGLEAFSRGKLGFTRSAGIT 145
Db 74 DHPIDYDDPKLEFEDHNYRKRILDKCKLEHGGEGLEESKGLKNGI-NTVDGAT 132
Oy 146 -YREMAPGAHSAALVGDENNMMNADWTTRDDYGVWEIFLNNADGSPALPHSRKVKRM 204
Db 133 IYREMAPAAQEAQOLIGEFNNMMNAGKMKDEKFGIWSIKI-SHANGKPAIPHSKVFRRF 191
Oy 205 DTPSGV-KDSISAMIKFSVQAPGEI--PENGIIYDDPEEKYVFOHOPKRPESLRYES 261
Db 192 RHGGAWWDRIPAWIRYATPDASKFGAPYDGVWDDPACERIVFKHPRPKPDAPRIYEA 251
Oy 262 HIGMSSPEKINSYANFRDEVLPRIRLGNVAVOIMAOEHSYVASFQVHTNFPAPSSR 321
Db 252 HVGMSGEFEVSTYRFPADNVLPRIKANNNTVQMAIMHSHSYASGHTVTFEAVSSR 311
Oy 322 FGTPEDLKSLIDRAHELGILLVMDIVHSHSSNNTDGLNGFD-GTDTH--YFHGGPRGHH 378
Db 312 SGTPEDLKYLVRKASHLGILRVMDIVHSHSNVNTDGLNGYDVGQNTHESEYFHTGDRGYH 371
Oy 379 WWWDSRLFRYSGNEVLRFLISNARKMLEEYKDFRPGVTSMYVTHHGQMTPTGNGYE 438
Db 372 KLMDSRLFRYANWEVLRFLISNARKMLEEYKDFRPGVTSMYVTHHGQMTPTGNGYE 431
Oy 439 YGFATDVAVVYLMVNDLIHGLHPDAVSGEDVSGMPFCCIYPDPGAGVDFRLMAV 498
Db 432 YFSLTDVDAIYVMMLANHMLHGLPBEATVADVSGMPLVCRPVDEGAGVDFRLMAI 491
Oy 499 ADKWTIELK-QGDESNKMDIVHTLTNRNMLEKCVTAESHDQALVGDKTITAFMLDKM 557
Db 492 PDRWIDYLNKEDRKMSMEIVOTLTNRRTYKECIAVAESHDOSIVGDKTITAFMLDKM 551
Oy 558 YDFMALDRSTPRIDGIALHKMIRLVMTGCGEYVNFNGNFGHEWIDDPFGPOTLP 617
Db 552 YTGMSDLOPASPTINGIALQKMIHPTMALGSDGYNFGNEGHEWIDDPFGPOTLP 605
Oy 618 TSKVLPGNNNSYDKCRRFEDIGADFLRYHMOEFDQAMOHLEBKYFMTSEHQVSRKH 677
Db 666 -----EGNNWSYDKCRRGMSLVDTDLRYKYNMAAFDQAMALHEEFLLSSKQIVSDM 660
Oy 678 EEDKVIIFERGLVFEVNFHWSNFPDYRVGCSRPGRKYKVALDSDALFGGFSLLHDVD 737
Db 661 EKDVIYFERGLVFEVNFHWSNFPDYRVGCSRPGRKYKVALDSDALFGGFSLLHDVD 720
Oy 738 YFTT-----EHPHNDNRRSFSVYTPSTAVY 764
Db 721 HFTSPGMEGVETNPNRNSFKVLSPPRTVAY 755
RESULT 3
GIGB_HUMAN STANDARD; PRT; 702 AA.
ID GIGB_HUMAN Q04446;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
  enzyme) (Brancher enzyme).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN 11
RS SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93216700; PubMed=8463281;
RA Thon V.J., Khalil M., Cannon J.F.;
RT "Isolation of human glycogen branching enzyme cDNAs by screening
  complementation in yeast."
```

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CC -1- FUNCTION: Required for sufficient glycogen accumulation. The
CC alpha 1-6 branches of glycogen play an important role in
CC increasing the solubility of the molecule and, consequently, in
CC reducing the osmotic pressure within cells.
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glycosidic linkages of
CC glycogen.
CC -1- PATHWAY: Glycogen biosynthesis; third step.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Highest levels found in liver and muscle.
CC -1- DISEASE: Defects in GBE1 are the cause of glycogen storage disease
CC IV (GSD-IV) [MIM:235001]; also known as Andersen's disease. GSD-IV
CC is a rare form of glycogenosis characterized by the accumulation
CC of abnormally structured glycogen that results in early onset
CC hepatic cirrhosis, cardiac arrest and neuromuscular diseases. Most
CC children with this condition die before two years of age. No
CC treatment apart from liver transplantation has been found to
CC prevent progression of the disease.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L07956; AAA58642.1; -.
CC PIR: A46075; A46075.
CC Genew: HGNC:4180; GBE1.
CC GK: Q04446; -.
CC MIM: 607839; -.
CC GO: GO:0003844; F:1,4-alpha-glucan branching enzyme activity; TAS.
CC GO: GO:0006091; P:energy pathways; TAS.
CC GO: GO:0005977; P:glycogen metabolism; TAS.
CC InterPro: IPR006477; Alpha_amy_cat.
CC InterPro: IPR004193; Glyco_hydro_13N.
CC Pfam: PF00128; alpha-amyase; 1.
CC Pfam: PF02922; Isoamylase N; 1.
CC DR Glycogen biosynthesis; Transferase; Glycosyltransferase;
CC KW Glycogen storage disease.
CC FT ACT_SITE 251 251 BY SIMILARITY.
CC FT ACT_SITE 286 286 BY SIMILARITY.
CC FT ACT_SITE 291 291 BY SIMILARITY.
CC FT ACT_SITE 355 355 BY SIMILARITY.
CC FT ACT_SITE 357 357 BY SIMILARITY.
CC FT ACT_SITE 412 412 BY SIMILARITY.
CC FT ACT_SITE 480 480 BY SIMILARITY.
CC FT ACT_SITE 481 481 BY SIMILARITY.
CC SQ SEQUENCE 702 AA; 80443 MW; 4DF3AABD365ABFE3 CRC64;
Query Match 51.3%; Score 2140; DB 1; Length 702;
Best Local Similarity 57.5%; Pred. No. 2,1e-150;
Matches 390; Conservative 102; Mismatches 170; Indels 16; Gaps 5;
Oy 89 KIYEIDPTLKDRSHLDYRSEYRIRAAIDHGGLEAFSRGKLGFTRSAGIT-R 147
Db 30 RLLEIDPYLKPAVDFQRKRYKQFSLKNGENEGGIDKFSGYESFGVRCADGGLYSK 89
Oy 148 EWAPGAHSAALVGDENNMMNADWTTRDDYGVWEIFLNNADGSPALPHSRKVKRM 207
Db 90 EWAPGAHSAALVGDENNMMNADWTTRDDYGVWEIFLNNADGSPALPHSRKVKRM 149
Oy 208 SG-VKDSISAMIKFSVQAPGEI--PENGIIYDDPEEKYVFOHOPKRPESLRYESHIGMS 266
Db 150 SGEIYRISPMKAYVREGDNVNTWIMHP--EHEYEKHSKSPKPRSLRIYESHIGIS 207
Oy 267 SPEPKINSYANFRDEVLPRIRLGNVAVOIMAOEHSYVASFQVHTNFPAPSSRFGTPE 326
Db 208 SHEKVASYKFTCVNLPRIKGLGYNCIQMAIMEHAYVASFQVHTNFPAPSSRFGTPE 267
327 DLKSLIDRAHELGILLVMDIVHSHSSNNTDGLNGFD-GTDTH--YFHGGPRGHH
```

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DB      268 ELQELVDTHASHWITVLLDVVSHASKNASDGLNMFDTGSCVHSGPRGTHIDMSRLP 327
QY      387 NYGSMWEVLRLSNARWMLBEYKFDGFRPDGVTSMTYTHGLQMTFTNGYGEYFGFATDV 446
DB      328 AYSSWEVLRLSNIRWMLBEYKFDGFRPDGVTSMTYTHGLQMTFTNGYGEYFGFATDV 387
QY      447 DAVVYMLVNDLHGLHPDVAISGEBVSQMPFTCIPTPDGSGVDYRLNMAVADKMTIEL 506
DB      388 DALTYMLNHLVHTLCQPSDITTAEDVSGMPALCSPISQGGGGRYRLNMAIPDKMTQL 447
QY      507 KQSDSWMKGDIVHTLNTNRWLEKCTYAESHDQALVGDITAFMLDKMDXDFMALDR 565
DB      448 KERKEDDMNGDVIYTLNTRRYLEKCIAYESHQALVGDYSLAFMLDMAMTMTSLT 507
QY      566 PSTPRIDRGIALHKMTRLVTMGLGEGYLNFMGNEFGHPENIDPPRGQTLPTGKVLPGN 625
DB      508 PFTPVIDRGIALHKMTRLVTMGLGEGYLNFMGNEFGHPENIDPPRGQTLPTGKVLPGN 556
QY      626 NNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEKYGFWTSEHOYYSRKHEEDKVIIF 685
DB      557 NESYHYARQFHLTDLLRYKFLNFDNRNLEBRYGWLAQAQAVSEKHGKILAF 616
QY      686 ERDDIVVFNEMHNSFPDPRVGSRGKYKVALDSDDALFGFSRLDHDYDPTTEHPH 745
DB      617 ERAGLFTFNFHPSKSTYDTRVGTALPGKFKVLDSDAAYGYGHORLDHSTDFSEAPEN 676
QY      746 DNRPSFSVYTPSRTAVY 763
DB      677 NGRPYLLVYIPRVALI 694

RESULT 4
GLGB_SOLUTU STANDARD; PRT; 861 AA.
AC P30924;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Starch branching
  enzyme) (O-enzyme).
DE SBE1 OR SBE.
OS Solanum tuberosum (Potato).
OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
  lamiales; Solanales; Solanaceae; Solanum.
OC NCBI_Taxid=4113;
OX RN
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Diabella;
RX MEDLINE=94105324; PubMed=8278528;
RA Poulsen P., Kreiberg J.D.;
RT "Starch branching enzyme cDNA from Solanum tuberosum.";
RL Plant Physiol. 102:1053-1054 (1993).

SEQUENCE OF 279-527 FROM N.A.
RP STRAIN=cv. Desiree; TISSUE=tuber;
RC MEDLINE=9207917; PubMed=1745241;
RA Kossmann J., Visser R.G.F., Mueller-Roeber B., Willmitzer L.,
  Sonnewald U.;
RT "Cloning and expression analysis of a potato cDNA that encodes
  branching enzyme: evidence for co-expression of starch biosynthetic
  genes.";
RL Mol. Gen. Genet. 230:39-44 (1991).
CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
  linkages in glycogen by scission of a 1,4-alpha-linked
  oligosaccharide from growing alpha-1,4-glucan chains and the
  subsequent attachment of the oligosaccharide to the alpha-1,6
  position.
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
  starch.
CC -1- PATHWAY: Starch biosynthesis; third step.
CC -1- SUBUNIT: Monomer.

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CC -1- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
-----
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-----
CC DR EMBL; X69805; CAA49463.1; -.
CC DR PIR; S34730; S34730.
CC DR InterPro; IPR006047; Alpha_amy1_cat.
CC DR InterPro; IPR004193; Glyco_hydro_13N.
CC DR Pfam; PF00128; alpha-amy1ase; 1.
CC DR Pfam; PF02922; isoamylase N; 1.
CC KW Starch biosynthesis; Transferase; Glycosyltransferase; Amyloplast;
  Chloroplast.
FT ACT_SITE 320 320 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
FT ACT_SITE 360 360 BY SIMILARITY.
FT ACT_SITE 427 427 BY SIMILARITY.
FT ACT_SITE 429 429 BY SIMILARITY.
FT ACT_SITE 484 484 BY SIMILARITY.
FT ACT_SITE 553 553 BY SIMILARITY.
SQ SEQUENCE 861 AA; 99083 MW; F3D519AC7C1BBF2 CRC64;

Query Match 50.9%; Score 2122.5; DB 1; Length 861;
Best Local Similarity 55.8%; Pred. No. 5,7e-149;
Matches 400; Conservative 97; Mismatches 189; Indels 31; Gaps 8;

QY 44 TAKLESSPPTGIVETITDGVTK-----GVKELVGEKRVVPKPGDGK---LY 91
DB 40 TGLKFGSQERSMIDISTPKSRVAKDERMKSSAISAVLTNDNGSMALBEDVKENIGLL 99
QY 92 EIDPTLKDFRSHLDVYSEYRIRRAAIDQEGGLEAFSRGKYLGFTRSAEGITYREMAP 151
DB 100 NIDPTLEPLLDHRHMKRYVDQKMLIEKYEGLPEBAQYLLKGFNRDCCIYREMAP 159
QY 152 GAHSAALVQDPNNWPNADTMTRDDYGVWEIFLPNNADSGPALFHGSRVKTMTDTPGV 210
DB 160 AAQEDDEVIGDFNGMNSNMHMEKDOFGWMSIRIP-DVDSKRVLPNHSRVKREFHGNGW 218
QY 211 KQISAMIKFSVQAQGEI--PENGIVDPPEEEKYVQCHQPKRPRESLRIYESHIGMSSP 268
DB 219 VDRIPAMIKATADATFPAAPVYDGVNDPPSERYHKKYRPPRPAPRIYEAHVGMSS 278
QY 269 EPKINSYANFRDEVLPRIKRLGYNAVOIMAIOESHYYASFGYHVTNFPAPSSRFETPDL 328
DB 279 EPRVNSYREPADVLPRIKANNNTVQLAIMESYSGFXYHTNFPAPSVSRGPNPDL 338
QY 329 KSLIDRAHELGVLVMDIVSHSSNNTLDGNGD---GDTYHYHGGRPRGHMMWDSRL 385
DB 339 KYLIDKXASHGLQVLDVAVVSHASNNTDINGDFDIQGSQESYFHAERGGYHKLWDSRL 398
QY 386 FNYGSMWEVLRLSNARWMLBEYKFDGFRPDGVTSMTYTHGLQMTFTNGYGEYFGFATDV 445
DB 399 FNYANWEVLRLSNLRWMLBEYKFDGFRPDGVTSMTYTHGLQMTFTNGYGEYFGFATDV 458
QY 446 VDAVVYMLNHLVHTLCQPSDITTAEDVSGMPALCSPISQGGGGRYRLNMAIPDKMTQL 505
DB 459 VDAVVYMLNHLVHTLCQPSDITTAEDVSGMPALCSPISQGGGGRYRLNMAIPDKMTQL 518
QY 506 LK-QSDSWMKGDIVHTLNTNRWLEKCTYAESHDQALVGDITAFMLDKMDXDFMALDR 564
DB 519 LKNNKNDWMSKRETSILNRYLEKCIAYESHQALVGDYSLAFMLDMAMTMTSLT 578
QY 565 RPTPRIDRGIALHKMTRLVTMGLGEGYLNFMGNEFGHPENIDPPRGQTLPTGKVLPGN 624
DB 579 TDASPVIDRGIALHKMTRLVTMGLGEGYLNFMGNEFGHPENIDPPRGQTLPTGKVLPGN 627
QY 625 NNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEKYGFWTSEHOYYSRKHEEDKVIIF 684

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DB 628 NMWYXKCRQWMLADSEHLRYKFMNAFDBRANSLDEKFSPLASGKQIVSSMDDNKVV 687

QY 685 FERGDVVFVFNPFVMSFPIRYVCGSPGKYKVALDSDDDALFGFSLDHDVDFTT 741

DB 688 FERGDVVFVFNPFVMSFPIRYVCGSPGKYKVALDSDDDALFGFSLDHDVDFTT 744

RESULT 5

GLGB_YEAST STANDARD; PRT; 704 AA.

ID GLGB_YEAST PRT; 704 AA.

AC 01-OCT-1993 (Rel. 27, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (glycogen branching enzyme).

GN GLC3 OR YEL011W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

NCBI_TaxID=4932;

SEQUENCE FROM N.A.

RP MEDLINE=92340578; PubMed=1634552;

RA Thon V.J., Vigneron-Lesens C., Marianne-Pepin T., Montreuil J., Decq A., Rachez C., Ball S.G., Cannon J.F.

RT "Coordinate regulation of glycogen metabolism in the yeast Saccharomyces cerevisiae. Induction of glycogen branching enzyme."

RL J. Biol. Chem. 267:15224-15228 (1992).

[2]

SEQUENCE FROM N.A.

RP STRAIN=S288C / AB972;

RA MEDLINE=97313264; PubMed=916968;

RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunnicutt-Smith S., Hyman R.W., Kayser A., Komp C., Laabkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petzel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.

RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V."

RL Nature 387:78-81 (1997).

CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucoacidic linkages of glycogen.

CC -1- PATHWAY: Glycogen biosynthesis; third step

CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING THE TRANSITION BETWEEN THE LATE EXPONENTIAL AND STATIONARY GROWTH PHASES, COINCIDENT WITH MAXIMAL GLYCOGEN ACCUMULATION.

CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC -----

CC EMBL: M76739; AAA3632.1; -

CC EMBL: U18530; AAB64488.1; -

CC PIR: S50449; S50448.

CC Germonline: 139015; -

CC SGD: S0000737; GLC3.

CC GO: GO:0003844; F.1.4-alpha-glucan branching enzyme activity; IGI.

CC GO: GO:0005977; P:glycogen metabolism; IMP.

CC InterPro: IPR006047; Alpha_amy1_cat.

CC InterPro: IPR004193; Glyco_hydro_13N.

CC Pfam: PF02922; isoamylase_N; 1.

CC Glycogen biosynthesis; Transferase; Glycosyltransferase.

CC ACT SITE 248 248 BY SIMILARITY.

CC ACT SITE 283 283 BY SIMILARITY.

FT ACT SITE 288 288 BY SIMILARITY.

FT ACT SITE 354 354 BY SIMILARITY.

FT ACT SITE 356 356 BY SIMILARITY.

FT ACT SITE 417 417 BY SIMILARITY.

FT ACT SITE 485 485 BY SIMILARITY.

FT ACT SITE 486 486 BY SIMILARITY.

FT ACT SITE 564 564 BY SIMILARITY.

FT CONFLICT 564 564 S -> T (IN REF. 1).

SC SEQUENCE 704 AA; 8115 MW; 9C227E107B825F27 CRC64;

Query Match 43.1%; Score 1795.5; DB 1; Length 704;

Best Local Similarity 51.4%; Pred. No. 6,6e-125;

Matches 367; Conservative 105; Mismatches 199; Indels 43; Gaps 17;

QY 84 PDDGQKIYEIDPTLDFRSHL-DYRYS-...YRIRALIDQHGGLAFSR-GYEKLGF 137

DB 5 PDNVGAVEFDWLPKPFADVLSEERYLADKMLYDITHTAPDGSQSKFAPDSKSYGL 64

QY 138 TRSAR-GITTYRWAPGASALVGFNNWNPNA-DTMRDDYGVWEIFLPNNADGSPAI 194

DB 65 HANPRTKEITTYKEMAPNARAFVGFNNWDTTSHLKNKDEGNFTTLHPLENGFPAI 124

QY 155 PHGRSVKIRMDTPSGVK-DSISAWIKFSVQAPGEI-----PNGIYDPPPEEKYVFOH 247

DB 125 PHDSKIKVFIIPDSKIFRLPAMITRATOPSKETSKQFGPAYEGRWNP-ENPYEFVH 182

QY 248 PPKRPE---SLRIYESHIGSSPEPKINSYANFRDEVLPRIKRLGNAYQVMAIQESHY 304

DB 183 PPKRSESVDLSRIYEAHVGISPEPKITTYKFTKVLPRIKVGLDALQVMAIMHAY 242

QY 305 YASFGYVTFNFPAPSRFRGTPEDLKLIDRAHELGLIVLMDIYHSHSNNTLDGLNGPDG 364

DB 243 YASFGYVTFNFPAPSRFRGTPEDLKLIDRAHELGLIVLMDIYHSHSNNTLDGLNGPDG 302

QY 365 TDTHYFHH-CGPRGHMMWDSRLFNYSWEVLRFLLSNARWMBEYKFGDFRFGVTSMM 422

DB 303 SHQYFHSISGRGEHPLDWSRLFNYSWEVLRFLLSNARWMBEYKFGDFRFGVTSMM 362

QY 423 YTHHGLQW-FTTGNAGEYFG--FATDVAVVYLMVNDLIQLHBD-AVSIQEDVSGM 476

DB 363 YVHGVGAGSGSGDYNELSNRDSFVDEHALYVLMADLVHMLPNAVTVADVSGY 422

QY 477 PFFCIIPVDPGVGFYRLMAVADKVIELIKQ-SDSWSKKGDIYHTITRMLKCTYTA 535

DB 423 PFLCIPRSIGTGFDFRLMALPDMWIKLIEKKDDEWEGSVYVITLNNRYGKVAVC 482

QY 536 ESHDQALVGDKTLAPFLMDKDY-DEMALDRPSTPRIDRGIALHKMRLVTMGSGSGYL 594

DB 483 ESHDQALVGDKTLAPFLMDKDY-DEMALDRPSTPRIDRGIALHKMRLVTMGSGSGYL 541

QY 595 NFMGNEFGHPWIDPFRGQTLPTGKVLPGNNNSYDKCRSRPFLGDADFLRYHMOEFDQ 654

DB 542 NFMGNEFGHPWIDPFRGQTLPTGKVLPGNNNSYDKCRSRPFLGDADFLRYHMOEFDQ 590

QY 655 AMQHLSEKYGFMSTSEKQYSRKHEDEKVIIFEGDVLVFNFMKSNFFDYRVCCSPGK 714

DB 591 SMQLOEKRRKNTKQAVYSLKHEGDKMVFEBNNMLFIENFPNTSYSDRVKVEKAGT 650

QY 715 YKVALDSDDALFGGFSRLDHDVDFTEHPDNRPRPSFYVTSRATVAVYALTE 768

DB 651 YKVALDSDDALFGGFSRLDHDVDFTEHPDNRPRPSFYVTSRATVAVYALTE 704

RESULT 6

GLGB_YIBVU STANDARD; PRT; 715 AA.

ID GLGB_YIBVU PRT; 715 AA.

AC Q8DGF0;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (glycogen branching enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-transferase).

GN GLGB OR VV21252.

```

OS  Vibrio vulnificus.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC  Vibrionaceae; Vibrio.
OX  NCBI_TaxID=672;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CIMC6;
RA  Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RT  Choy H.E.;
RL  Complete genome sequence of Vibrio vulnificus CMCP6."
Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
CC  linkages in glycogen by scission of a 1,4-alpha-linked
CC  oligosaccharide from growing alpha-1,4-glucan chains and the
CC  subsequent attachment of the oligosaccharide to the alpha-1,6
CC  position (By similarity).
CC  -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
CC  glycogen.
CC  -1- PATHWAY: Glycogen biosynthesis; third step.
CC  -1- SUBUNIT: Monomer (By similarity).
CC  -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC  -----
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CC  -----
DR  EMBL; AB016812; AAC08146.1; -.
DR  HAMAP; MF_00685; -; 1.
DR  InterPro; IPR006589; Alp_amy1_cat_sub.
DR  InterPro; IPR006047; Alpha_amy1_cat.
DR  InterPro; IPR006407; G1GB.
DR  InterPro; IPR004193; Glyco_hydro_13N.
DR  Pfam; PF00128; alpha-amylose; 1.
DR  Pfam; PF02922; isoamylase_N; 1.
DR  SMART; SM00642; Aamy; 1.
DR  TIGRFAMs; TIGR01515; branching enzym; 1.
KM  Glycogen biosynthesis; Transferrase; Glycosyltransferase;
KM  Complete proteome.
FT  ACT_SITE 291
FT  ACT_SITE 291
FT  ACT_SITE 326
FT  ACT_SITE 331
FT  ACT_SITE 331
FT  ACT_SITE 331
FT  ACT_SITE 394
FT  ACT_SITE 396
FT  ACT_SITE 449
FT  ACT_SITE 516
FT  ACT_SITE 517
SQ  SEQUENCE 715 AA; 81927 MW; 304C61BECF5A5F43 CRC64;
Query Match 15.1%; Score 628; DB 1; Length 715;
Best Local Similarity 25.3%; Pred No. 1.6e-38;
Matches 198; Conservative 138; Mismatches 289; Indels 158; Gaps 28;

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```

DB  243 G-SWKRNEQGEFLNRELAELVPLVDGTYHVEIMPVSEHPFYSGWQVQVGLFAPTS 301
QY  321 RFGTPEDLKSLIDRAHEGLVLLMDYHSHSSNNTLDGNGFGTDTHYHGGRGHMM 380
DB  302 RYGSDDDFKFEVDACHQAGIGVLLDWVPAHFPSDD-HGLANFGDTPLPHDDPRRGHND 360
QY  381 WDSRLFNVSWEVFLPLSNARWLEEKFKDGRFPDVTSMYTHGLQMTFTNGYGEYF 440
DB  361 WMSFYDLRGQVRRRLVSNALYMFQPHDGRVAVASMLX-----LDYSSHQWMI 414
QY  441 ----GRAVDVAVYVLMVNDLHGLHPAVSIGEDVSGMPTFCIPVDDGVGFYRLHM 496
DB  415 PMMDGENENYDALATLKMNEEYKYFPNMTIAESTAFPGVSAFTFMGLGFGFKMM 474
QY  497 AVADKTELLKQSDSESKGDIYHTLTNRKLEKCTYAE-----SHDQALVQKTI 548
DB  475 GWMHDSLSYIKE-----EPVARKYHNTLTFPLVYASENVYLSLSDHEVYGGKSI 526
QY  549 -----AFYLMKMDVDFMALDRPSTPRIDRGIALHKIRLVTMGLGEGY-----L 594
DB  527 HNMPEDEWQQTANLAIYF-----GYMGOQPKKL 556
QY  595 NFMGNFEGH-PWIDPEPRGFQTLPTGKVLPGNNNSYDKRRRFDLADPLRYHGMQEPD 653
DB  557 NFMGALIGQTAEW-----NHDDQIQWFL-----DPRHGOVQALY 592
QY  654 QANQHLLEEKYGFMTSE-----HQYYSRKHEKDKVILFER-----GDLVFVNFMSNFF 703
DB  593 RDLNHLRYNQAALHDQCI PAGFEWRLODAEOSTIAHERSEAGERLVVSNFTPVPRD 652
QY  704 DYRVGSGRGKYVVALDSDPALDGFGRFLDHDVYFTTEPHDNRPRFSYTSRTAVV 763
DB  653 EEPFLGVPNKRQYQLLNTDSTKTAQ-SGEVYVDKAEAVSEDLAQSVLRPLPLSLTF 711
QY  764 YAL 766
DB  712 YKL 714

```

RESULT 7
ID GLGB SYNPF STANDARD; PRT; 773 AA.
AC P16954;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (glycogen branching enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyltransferase).
DE GLGB.
OS *Synechococcus* sp. (strain PCC 7942) (*Anacystis nidulans* R2).
OC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90333609; PubMed=2142668;
RA Kiel J.A.K.W., Boels J.M., Beidman G., Venema G.;
RT "Nucleotide sequence of the *Synechococcus* sp. PCC7942 branching enzyme gene (glgB): expression in *Bacillus subtilis*,"
RL Gene 89:77-84 (1990).
CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic linkages in glycogen by scission of a 1,4-alpha-linked oligosaccharide from growing alpha-1,4-glucan chains and the subsequent attachment of the oligosaccharide to the alpha-1,6 position (By similarity).
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of glycogen.
CC -1- PATHWAY: Glycogen biosynthesis; third step.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS APPROXIMATELY 35 DEGREES CELSIUS.

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 CC
 CC EMBL, M1544; AAB39038.1; -.
 DR PIR: J00550; J00550.
 DR HAMAP: MF_00685; -; 1.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR006407; GlgB.
 DR InterPro: IPR004193; Glyco_hydro_13N.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR Pfam: PF02922; isoamylase N; 2.
 DR TIGRFAMs: TIGR01515; branching_enzym; 1.
 DR Glycogen biosynthesis; Transferrase; Glycosyltransferase.
 KM INIT_MET 0
 FT ACT_SITE 334 334 BY SIMILARITY.
 FT ACT_SITE 369 369 BY SIMILARITY.
 FT ACT_SITE 374 374 BY SIMILARITY.
 FT ACT_SITE 437 437 BY SIMILARITY.
 FT ACT_SITE 438 438 BY SIMILARITY.
 FT ACT_SITE 492 492 BY SIMILARITY.
 FT ACT_SITE 559 559 BY SIMILARITY.
 FT ACT_SITE 560 560 BY SIMILARITY.
 SQ SEQUENCE 773 AA; 89063 MW; 52BA117CA337BF57 CRC64;

Query Match 15.08; Score 624; DB 1; Length 773;
 Best Local Similarity 24.9%; Pred. No. 3.5e-38;
 Matches 198; Conservative 111; Mismatches 249; Indels 238; Gaps 32;

75 GKKPRVYVPPKPGDQKYEI-DPTLKDFRSLHDVRSYRRIRAIIDHSGLEAFSGYE 133
 DB GERERTIYD-----YAFRSPLITDIDIL-FAGGNHRI-----YE 132
 134 KLGF-----TRSAEGITYREWAPGASALYGVDFNNMNPADDTMRDYGVWEIPLP- 185
 133 KGAHPCELENVAGVAFVAPSAFARNVSIIGDFNSWDGRKHQARRSGIETLPELTIV 192
 186 -----NNAAG-----SPAIFGSRVYKIMDPGSGVSDISAMIKFSVQAFGEIIPNGIT 234
 193 GAAYKEIKNYDGHIEKSDPYGQOEVRPKTASIVADL----- 231
 235 YDPEEEKYVF-----QHPOKRPESLRIRIYESHIG-----MSSPEPK 271
 232 -----DRITWGDADMLERRRHOEPLR-QPISVTEVHLGSMHASSDAIATDAOGKPLP 284
 272 IN-----SYANFDEVLPRIRKLGNAYQVIAIOESYASRGYAVTFFAPSS 320
 285 VPADILKPGARFLTYRELADRLIPYVDLQSHIELPIAHPPDGGSGYVLTGYVATLS 344
 321 RRGTPBDKSLIRPAHEGLJLVMDIYHSHSSNNLTDLQNGFDGDTDTHYFHGGRGHHMM 380
 345 RGSPPDFMFVVRCHONGIGVILDWPGHFKPGG-HGLAFDGTTHUYEHADSQGEHRE 403
 381 WPSRLFNYSGWSEWELRFLLSNARMKLEEKYKDPGFPDGYTSMNYHHGLOMFTGNQYGEY 439
 404 WGLTVNNGGHEVRNFIANALFWFDKXHTDGIIVDAVASMLY-----LQYNRKEGEMT 457
 440 ---FGFATDVAVVYLYLVNDLHGLHPDAVSGEDVSGMPTFCIPYDGGVGFDYRLHM 496
 458 PNEYGGRRENIEADFLRGVNHILFSYFGALSIABESGSMWMPVTVGLGFTLK--- 514
 497 AVADKTIELLKQDDESWKMGDIYHTLNNRRLEKCVTYABSHD---QALVDKTIATFALM 553
 515 -----WNMG-----WMHMDLYFMSDPWFRQFHONNVTFISIVYA 548
 554 DKDMYDFMALDRPSTPRIDRGIALHKYIRLYVTMGLGSE-----GVL----- 594

595 NFMNGEHPHPEWIDPRPGDQLPTGKVLFGNNNSYDKCRRRFDLGNADF-LRY--HGM 649
 DB LFMGHEFG--QWAEW-----NW-----GDLEWHLQYEPHQGL 631
 650 QEPDQAMHLEKRYEPMTSE-----HQYVS---RKHEEDKVIIFERGD 690
 DB KQFVNDLNLIRNAPALYSDEDNQAGFEWIDCSDNRHASIVSFTRRHESDR?-----L 684
 691 VFVFNFMNSHFDRVCGSRPGKYKVALDSDDALFGGFSRLDHDVDPYPTTEHPDNRPR 750
 DB VVVCNF-TPQRAHRIQVPAVGFRERINSDASVGG-SMNGNLGKKTWDEMSCHNRPY 742
 751 SPSVYTPSRITAVVAL 766
 DB SLUDLCPPLTIVLEL 758

RESULT 8
 GLGB_VIBPA STANDARD; PRT; 755 AA.
 ID GLGB_VIBPA
 AC Q87FR0;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-transferase).
 DE GLGB OR VPA1618.
 GN Vibrio parahaemolyticus.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrrio.
 OC NCBI_TaxID=670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RMD 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shingawa H., Hattori M., Iida T.;
 RA "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";
 RL Lancet 361:743-749 (2003).
 CC -!- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic linkages in glycogen by scission of a 1,4-alpha-linked oligosaccharide from growing alpha-1,4-glucan chains and the subsequent attachment of the oligosaccharide to the alpha-1,6 position (By similarity).
 CC -!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of glycogen.
 CC -!- PATHWAY: Glycogen biosynthesis; third step.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC
 CC EMBL, AP005089; BAC62961.1; -.
 DR HAMAP: MF_00685; -; 1.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR004193; Glyco_hydro_13N.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR Pfam: PF02922; isoamylase N; 1.
 DR Glycogen biosynthesis; Transferrase; Glycosyltransferase;
 KM Complete proteome.
 FT ACT_SITE 330 330 BY SIMILARITY.
 FT ACT_SITE 365 365 BY SIMILARITY.

FT ACT_SITE 433 433 BY SIMILARITY.
FT ACT_SITE 435 435 BY SIMILARITY.
FT ACT_SITE 488 488 BY SIMILARITY.
FT ACT_SITE 555 555 BY SIMILARITY.
FT ACT_SITE 556 556 BY SIMILARITY.
SQ SEQUENCE 755 AA; 87504 MW; 8F052368B657D79 CRC64;

Query Match 14.9%; Score 620; DB 1; Length 755;
Best Local Similarity 25.4%; Pred. No. 6.6e-36;
Matches 193; Conservative 133; Mismatches 273; Indels 174; Gaps 30;

QY 71 ELVVGKPRV-VKPKDGOKIY--EIDPTLKDFRSHLDYR-----YSEYR 112
DB 78 ELVNGEPVALERDSDSGFLKEGRDLHLHYLADVAMNVEQIIDPYQYHNYGEYE 137
QY 113 RIRALIDQHE--GGLPAFSGYEKLGFTRSAGGITYREMAPGASALVGDENNANNA 169
DB 138 HLHTPKDMHYMGAAHFTLERGGENI-----SGVRFVYAPHASAVSLVGCFCFQMDGR 191
QY 170 DMTTRDDYGWEIFLNNADSPALPHGSRKIMDPS--GVKDSISAMIKFSVQAPGE 227
DB 192 HPMQRDLGYGIGLFT-----PGLERGVQYKFKLKGPNHGGLPKKDPMGFTSEQYFS 243
QY 228 IPFNGIYDDPEEEKYVFOHPQ-----PKRPSRLRYESHIGMSPEPKINSYANFR- 279
DB 244 --FASTYD--HKRYOMQAKMKNRAVTCRDEALSFYELHAGSWKRGK-GDFLNYRE 297
QY 280 --DEVLEIRIKLGNAVQIAIQSHSYASGCHVNTFPAQSGFPTEDLSLIDRAHE 337
DB 298 LABQLVYLVDMGYTHLMFVSHSPFGSGWQYQVGFAPTSRYSQSDDFEFVADACHQ 357
QY 338 LGLVLMIDYHSHSNNTLDGDFDGDTHYFGSGPRGHMMMSRLFNYSMEVLEPL 397
DB 358 AGGIVGVLDWVPAHPSPDD-HGLANFDGTLPHDPDRRHGMODMNSYIYDGLREHVRFL 416
QY 398 LSNARWMLSEYKFGFRPDVTSNMYTNGLOMTFTGNYGEYF--GFADVDAVVYLM 453
DB 417 VSNRLYFEGQHDGIRVDAVASMLY-----LDVSRSHDQVPRVVDGNNENYDALTLK 470
QY 454 LVNDLHGLHPDAVISIGDVSGMPTCTPVDGQVGEPRYRLMAVADKRIELKQSDSW 513
DB 471 WMNEEYVKHFNAMNTIAEESTAFPGVSAFTPMGGIGFGFKNMWG--WM--HDSLSY 522
QY 514 KMGDIYVTLNRRRLKLVTAE-----SHDQALGDKTI-----APFLMKDM-- 557
DB 523 VKEDPRVKYHNNHTTTPLVYAHSENYVLSHSDVVGKGSINNMKPEDENQOQANLPA 582
QY 558 --YDFMADRPSTPRIDRGIALHKMIRLVMTGLGSEYVNFQNEFGH--PEWIDFRPGPOT 615
DB 583 YTGIM-----YQGPGR-KLNFMAELGQTNEM----- 608
QY 616 LPTGKVLPGNNNSYDKCRRRPDLGDADLRLYHGMQEPDQAMQHLBEKFGFMSHGYSR 675
DB 609 -----NHDDQLQWFLD--EYERHOGVQKLMKMDLNLHLYRNEAM----- 644
QY 676 KHEED-----KVILFER--GDLVFVNFMSNSFPDYRVCGRSGRKY 715
DB 645 --HDDCCVPAGEWRMLQDEADASITLHAKISKEGELLITNTTPVPHHEFRIGVPRVGOY 703
QY 716 KVALDSDALFGG--FSRLDHDVDYFTTEHPRHNPSPSVYTPSRTAVVVAL 766
DB 704 ELLANTDSKKGSGSPKVL---TSVTKERKVESBSLPGSLLELLPLSLTYFYKL 753

RESULT 9
GLGB_VIBCH STANBARD; PRT; 666 AA.
ID GLGB_VIBCH
AC Q9KNE8;
DT 10-OCT-2003 (Rel. 42, Last Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1.4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching

DE (transferase).
GN GLGB OR VCA0016.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.P., Eissen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bae S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Ueberback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Frazer C.M.,
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae".
RL Nature 406:477-483 (2000).
CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
CC linkages in glycogen by scission of a 1,4-alpha-linked
CC oligosaccharide from growing alpha-1,4-glucan chains and the
CC subsequent attachment of the oligosaccharide to the alpha-1,6
CC position (by similarity).
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
CC glycogen.
CC -1- PATHWAY: Glycogen biosynthesis; third step.
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL: AE004345; AAP95930.1; --
CC PIR: D82511; D82511.
CC TIGR: VCA0016; --
CC HAMAP: MF_00685; atypical; 1.
CC InterPro: IPR006047; Alpha_amyl_cat.
CC InterPro: IPR006407; G1GB.
CC InterPro: IPR004193; Glyco_hydro_13N.
CC Pfam: PF00128; alpha-amylase; 1.
CC Pfam: PF02922; isoamylase; 1.
CC DR TIGRGRAMS; TIGR01515; branching_enzyme; 1.
CC KM Glycogen biosynthesis; Transfeferase; Glycosyltransferase;
CC complete proteome.
CC FT ACT_SITE 240 240 BY SIMILARITY.
CC FT ACT_SITE 275 275 BY SIMILARITY.
CC FT ACT_SITE 280 280 BY SIMILARITY.
CC FT ACT_SITE 343 343 BY SIMILARITY.
CC FT ACT_SITE 345 345 BY SIMILARITY.
CC FT ACT_SITE 398 398 BY SIMILARITY.
CC FT ACT_SITE 465 465 BY SIMILARITY.
CC FT ACT_SITE 466 466 BY SIMILARITY.
SQ SEQUENCE 666 AA; 77095 MW; BA538EBD93DE9868 CRC64;
Query Match 14.2%; Score 592.5; DB 1; Length 666;
Best Local Similarity 25.4%; Pred. No. 6e-36;
Matches 171; Conservative 122; Mismatches 238; Indels 143; Gaps 25;

QY 108 YSEYRIRALIDQ--HEGGLPAFSGYEKLGFTRSAGGITYREMAPGASALVGDENNANNA 166
DB 43 YAEYEDLHTPKQMYHNGAOFVT--LERDG--KVVSGVRFVYAPHASAVSLVGCFCFQMDGR 98
QY 167 PNADYTRDDYGWEIFLNNADSPALPHGSRKIMDPS--GVKDSISAMIKFSVQAPGE 224
DB 99 GRNHQRLDYGIGLFT-----PGLERGVQYKFKLKGPNHGGLPKKDPMGFTSEQYFS 151

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QY 225 PGEIIFNGIYYDPPEBEKYFQ---HPQ---KREPSIRIYSHIGSSPEPKINSYAN 277
D 152 PS---FAVITYD---HRRYQWODTAMQGRPVTEKRKQALSFELHYG-SWKEGENSEFLN 204
QY 278 FR---DEVLPRIKELGYNAVQIMAIQEHSYASFGYHVTNFFAPSSRFGEPELXLIDR 334
D 205 YRELADQVLPYLVEGYHVELMPVAHEHPFGYSWGQVPGVLFAPTSRQSPDDFKITVDL 264
QY 335 AHELGLVLMIDIVHSHSNNTLDGLNGFQDTTHYFGGPRGHMMWDSRLFFYGSWEVL 394
D 265 CHQAGIGVLDVNPVHPFSDS-HGLANFQGTPLFHPDPRRGHQMOMNSIYVLGEHNR 323
QY 395 RFLLSNARWLEBYKFGDFRFDGVTSMYTHGLQMTFTGNYGEYF---GFATDVAVY 450
D 324 RFLVANALYWFEMFHDIGIRYDAVASMLY-----LDYGRSHDQMTPNVDGGRNEDALA 377
QY 451 YLMLVNDLHGHPDAVSGEDVSGMPTCIPYPDGCGVFDYRLHNAVADKMTELKQSD 510
D 378 TFKWNNBZYKFPFPAAMTAEESTAPGVSAPTFMGGLGFGFKMNGMMHDSLYKE-- 435
QY 511 ESMKMGDIYHTLTJNRWLEKCTYA-----ESHQALVGDXTAF-----WIMDKD 556
D 436 -----DVRHRYHNTLTPLLIYAFSENYVLSLSDDEVYGRSLMYKRPDEMOQTAN 469
QY 557 MYDEVALDRPSTPRIDRGIALHMKTRLVTMGLGEGY-----LNFMGNEFGH-PEWT 607
D 490 LRAYL-----GYMTGQPGKILNFMQTELGQTAEW- 518
QY 608 DFPKPGQTLPTKVLPGNNNSYDKCRRRFDLGDADLRLHNGMEFQOAMHLEBKGFMT 667
D 519 DHDGQLQWFLT-----QPERHAGIGRLVYDLNHL---YQAOQ 552
QY 668 SEHQ-----YYSRKHEEDKVIIFER---GDVVFVFNFMNSFFDYRVCSSBPX 714
D 553 ALHQJLDCDPRGEMRLQDNADLSVIAHERMDEKGNVLTNTPTVPQCEFRIGVPKTXG 612
QY 715 YKVALDSDALFPG 728
D 613 YRLINTAKQYNG 626
RESULT 10
GLGB_NITEU STANDARD; PRT; 734 AA.
AC 081ZU6;
D 10-OCT-2003 (Rel. 42, Created)
D 10-OCT-2003 (Rel. 42, Last sequence update)
D 10-OCT-2003 (Rel. 42, Last annotation update)
D 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
  transferase) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-
  transferase).
  GLGB OR NE029.
  Nitrosomonas europaea.
  Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
  Nitrosomonadaceae; Nitrosomonas.
  NCBI_Taxid=915;
  [1]
  SEQUENCE FROM N.A.
  STRAIN=ATCC 19718 / IPO 14298;
  RX MEDLIN=22866410; PubMed=12700265;
  RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
  Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
  Arciero D.M., Holmes N.G., Wlitzaker M.M., App D.J.;
  "Complete genome sequence of the ammonia-oxidizing bacterium and
  RT obligate chemolithoautotroph Nitrosomonas europaea."
  J. Bacteriol. 185(12):2759-2773(2003).
  -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
  linkages in glycogen by scission of a 1,4-alpha-linked
  oligosaccharide from growing alpha-1,4-glucan chains and the
  subsequent attachment of the oligosaccharide to the alpha-1,6
  position (by similarity).
  -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
  glycogen.
```

```
CC -1- PATHWAY: Glycogen biosynthesis; third step.
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; BX321863; CAD85940.1; -.
DR HAMAP; MF_00685; -; 1.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006407; GLGB.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR Pfam; PF00128; alpha-amyase; 1.
DR Pfam; PF02922; isoamyase_N; 1.
DR SMART; SM00642; Aamy; 1.
DR TIGRFAMs; TIGR01515; branching enzym; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
  Complete proteome.
FT ACT_SITE 308 BY SIMILARITY.
FT ACT_SITE 343 BY SIMILARITY.
FT ACT_SITE 348 BY SIMILARITY.
FT ACT_SITE 411 BY SIMILARITY.
FT ACT_SITE 413 BY SIMILARITY.
FT ACT_SITE 466 BY SIMILARITY.
FT ACT_SITE 533 BY SIMILARITY.
FT ACT_SITE 534 BY SIMILARITY.
SQ SEQUENCE 734 AA; 84101 MW; AFD8499CJA45EE4 CRC64;
Query Match 13.9%; Score 579; DB 1; Length 734;
Beet Local Similarity 26.0%; Pred. No. 6.9e-35;
Matches 188; Conservative 103; Mismatches 257; Indels 176; Gaps 29;
D 106 YRYSEYRIRAIIDQHEGLBAFSGYEKLGFT---SASGITREMAPGAHSAALVGD 161
D 115 YLFNIEGRLLQ-----YHMLGHRVNRHCVGTGRFPAVMNRERGVSGD 159
QY 162 FNNNPNNA-DTMTDDVGVWEIPLFNADGSPALPHGSRVYKRMTPSGVKSISMIKX 220
D 160 FNRWDGRVYPMVNVHSGVWEIPLD-----LDEGALYKYE-----IRNRIS----- 201
QY 221 SVQAPGEI-----PENGIVYPRPE-----BEKYVFOHQ---PKRP-----ESTRIYE 260
D 202 -----GELLKTDPAATYELRPNNALPTLPBQKTDKDDMIARKGMDMLHAPLNIYE 256
QY 261 SHIG-MSSPEPKINSYANFRDEVLPRIKRLGYNAVQIMAIQEHSYASFGYHVTNFFAP 318
D 257 LHVSGMKRHPDGRFYSYHDLADHLIPYLDKMGYSVELLPISBHPDSEMGVATGVFAV 316
QY 319 GSRFGTEPDLKSLIDRAHELGLVLMIDIVHSHSNNTLDGLNGFQDTTHYFGGR-GR 377
D 317 TSYRGSPFAFMSFVDRCHQAGIGVILDWPAFPODSF-SLARFDGT-ALYEHEDPRLGY 374
QY 378 HMMWDSRLFFYGSWEVLAEFLSNARWLEBYKFGDFRFDGVTSMYTHGLQMTFTGNYG 437
D 375 HHMDGTLYFNNGRNEVKSFLLSSAHYWSAFHTDGLRDAVASMLY-----LNTSRKEG 428
QY 438 EY-----GFATDVAVVYLMVNDLHGHPDAVSGEDVSGMPTCIPYPDGCGVFDYR 493
D 429 EMLNRYGHNHLEBILRLANMTWVHGEPALFPAESTSWPAVSRAVYGLGFSMK 488
QY 494 LHMVADKVELIKOSDSSKMGDIYHTLTNRWLEKCTYAE-----SHDQA 541
D 489 WNMG-----WM-----NDLSTYMOCHDPVH---RRYHNEELTFQOLVAYTENFVLPLSHDEV 536
QY 542 LVGDKTIAFWLMDKMDVPMALDRPSTPRIDRGIALHMKIRLV---TMGLGEGYLNFMG 598
D 537 VHGRKS-----MLDKRPGD-----GWQKFAVRLILFTYQMTCPGK-KTNFMG 577
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GN GLGB OR MUR7587.
 OS Rhizobium loti (Mesorhizobium loti).
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Phyllobacteriaceae; Mesorhizobium.
 CX NCBI_TaxId=381;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFR30309;
 RX MEDLINE=21082930; PubMed=11214966;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Matsubara A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
 Takeuchi C., Yamada M., Tabata S.,
 RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti";
 RL DNA Res. 7:331-338(2000).
 CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
 CC linkages in glycogen by scission of a 1,4-alpha-linked
 CC oligosaccharide from growing alpha-1,4-glycan chains and the
 CC subsequent attachment of the oligosaccharide to the alpha-1,6
 CC position (By similarity).
 CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
 CC glycogen.
 CC -1- PATHWAY: Glycogen biosynthesis; third step.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC or send an email to license@ebi.ac.uk).
 CC
 CC -----
 CC EMBL: AF003012; BAB54018.1; -
 CC DR HAMAP: MF_00685; -1.
 CC DR InterPro: IPR006047; GLGB_alpha1_cat.
 CC DR InterPro: IPR006047; GLGB.
 CC DR InterPro: IPR004193; Glyco_hydro_13N.
 CC DR Pfam: PF00128; alpha-amy1ase; 1.
 CC DR Pfam: PF02922; isoamylase N; 2.
 CC DR TIGRFAMs: TIGR01515; branching enzyme; 1.
 CC KM Glycogen biosynthesis; Transferrase; Glycosyltransferase;
 CC Complete proteome.
 CC
 CC FT ACT_SITE 314 BY SIMILARITY.
 CC FT ACT_SITE 349 BY SIMILARITY.
 CC FT ACT_SITE 354 BY SIMILARITY.
 CC FT ACT_SITE 417 BY SIMILARITY.
 CC FT ACT_SITE 419 BY SIMILARITY.
 CC FT ACT_SITE 472 BY SIMILARITY.
 CC FT ACT_SITE 539 BY SIMILARITY.
 CC FT ACT_SITE 540 BY SIMILARITY.
 CC FT ACT_SITE 540 BY SIMILARITY.
 CC SQ SEQUENCE 737 AA; 82525 MW; BF8BCAID72A8AAB CRC64;
 CC
 CC Query Match 13.8%; Score 574; DB 1; Length 737;
 CC Best Local Similarity 25.7%; Pred. No. 1,6e-34;
 CC Matches 182; Conservative 101; Mismatches 240; Indels 184; Gaps 27;
 CC
 CC 91 YEIDPTLKDFRSHLDYRYS-----YRIRALDQHEGLAEFRGKYGFTRSAGI 144
 CC 109 YSRGVPVLGPD--DYIAEGSHLRLEPKLGAHYIEHEG-----ATGV 148
 CC
 CC 145 TYREAFPGASALVGDFFNNMNNADTM--TRDYGVEIFLPPNADSP-----ALPHGS 198
 CC 149 HFVWMPNKRKRVSVGDGFNDMDGRHRTMRDRDGIWEVFLPDIGARPKYKYEITGPQGV 208
 CC 199 RVKIRMDTSGVSDISAWIKFSVQAGELPENGIIYDPPREKKYVQHPQKPESLRI 258
 CC 209 RLPKRD--PFAFSELRPAFASVAVAPADWG-----DEAHNYMRNADPR--EAVSI 260
 CC 259 YESHIG--MSSPEPKINSYANFDEVLPRIKRLGYNAVQIWAQEHSHSYVASFGYHTNPF 316

DB 261 YEVAHGSQQLHDDGTGLSWDELADRLIPVETGTFHLEFMRISHEPDPBSKGYQTGLY 320
 CC
 CC 317 APSRFGTPEDLKSLIDRAHEGLVLVMDIVSHSSNNLTLDGIAGDGTDTYFHGPR- 375
 CC 321 APSARFGDPDGFARVDDGAHARGVILLDWVAHPVDA-HGLAHPDGT-ALYEHADPRK 378
 CC
 CC 376 GHEMMWDSRLFNYSWEVLRFLSNARWMLBEYKPDGFRFDGYSMMYTHHGLOMTGN 435
 CC 379 GFHPDMNTALYNFGREEVASFLVNNALFWAEKXHYDGLRVDAVASMLY-----LDYSRK 432
 CC
 CC 436 YGEYF-----GATVDVAVVYMLVNDLJHGLHPDAVSIGEDYSGMPTFCIPVDDGVGFD 491
 CC 433 AGEWTPNEKGRRENLEAVSFLQKMKKEYGHHGPVNTIAESTSWPKVASAPVEHGLGFG 492
 CC
 CC 492 YRLHVAVADKWIETLLKQDSRWKMDIVTTL-----NRMLEKCVTYA----- 535
 CC 493 FK-----WNGFMHDTLEYFSKEPIFRKHNNLDLFRGLTYAFSENF 533
 CC
 CC 536 ---ESHQALVGDKTIAFWLMDKMYDEMALDRPSTPRIDRGIALHKMRLVTMGLOGEG 592
 CC 534 VLPASHDEVVHGKGTLLSKMAGDDWQKF-----ATLRAYYGF-----NMGYPGKK 578
 CC
 CC 593 YLNPFGNFFG--HPEVIDPPRGQTLPTGKVLPGNNNSYKCRRPDLGDADFLRYHMOE 651
 CC 579 LL-FMGQEPFAQRREWS-----AALDWMLDPRPHRGVW- 612
 CC
 CC 652 PDQAMCHLEKXGPFMTSHQVSRKHEDEKVIIFERGLVFFVNFPM-----SNSEFF- 703
 CC 613 --QYVRDLNLYRSKPAHL--GRCEPE-----GFWMILYDSDQNSVFAW 653
 CC
 CC 704 -----DYNGCSRFGKRYKALDSDDALFEG 728
 CC 654 VRNAPGSPVAVISNFTVPVRDNYRVPLPKAKWEHIIINTDASEYGG 700
 CC
 CC RESULT 13
 CC GLGB SYN3 STANDARD; PRT; 770 AA.
 CC AC P52981;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE 1,4-alpha-Glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
 CC enzyme) (BS) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-
 CC transferase).
 CC DE GLGB OR S1L0158.
 CC GN Synecocystis sp. (strain RCC 6803).
 CC OS Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 CC OX NCBI_TaxId=1148;
 CC RN
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=96127529; PubMed=8590279;
 CC RA Sugita M., Tanaka A., Sato S., Kocani H., Saruka T., Miyajima N.,
 CC Kaneko T., Tabata S.,
 CC "Sequence analysis of the genome of the unicellular cyanobacterium
 CC Synecocystis sp. strain RCC6803. I. Sequence features in the 1 Mb
 CC region from map positions 64k to 92k of the genome.",
 CC DNA Res. 2:153-166(1995).
 CC RL
 CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
 CC linkages in glycogen by scission of a 1,4-alpha-linked
 CC oligosaccharide from growing alpha-1,4-glycan chains and the
 CC subsequent attachment of the oligosaccharide to the alpha-1,6
 CC position (By similarity).
 CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
 CC glycogen.
 CC -1- PATHWAY: Glycogen biosynthesis; third step.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC or send an email to license@isb-sib.ch).

CC EMBL: D63999; BAA10073.1; --
 CC PIR: S76095; S76095.
 CC HAMAP: MF_00685; --; 1.
 CC InterPro: IPR006047; Alpha_amy1_cat.
 CC InterPro: IPR006407; GlbB.
 CC InterPro: IPR004193; Glyco_hydro_13N.
 CC Pfam: PF00128; Isoamylase; 1.
 CC Pfam: PF02922; Isoamylase N; 2.
 CC TRFPMs: TIGR01515; branching_enzym; 1.
 CC Glycogen biosynthesis; Transferrase; Glycosyltransferase;
 CC Complete proteome.
 CC ACT_SITE 328 BY SIMILARITY.
 CC ACT_SITE 363 BY SIMILARITY.
 CC ACT_SITE 368 BY SIMILARITY.
 CC ACT_SITE 431 BY SIMILARITY.
 CC ACT_SITE 431 BY SIMILARITY.
 CC ACT_SITE 433 BY SIMILARITY.
 CC ACT_SITE 486 BY SIMILARITY.
 CC ACT_SITE 553 BY SIMILARITY.
 CC ACT_SITE 554 BY SIMILARITY.
 CC ACT_SITE 554 BY SIMILARITY.
 CC SEQUENCE 770 AA; 89527 MW; A435AFCAT703FA8A CRC64;

Query Match 13.7%; Score 573; DB 1; Length 770;
 Best Local Similarity 25.2%; Pred. No. 2e-34;
 Matches 191; Conservative 103; Mismatches 271; Indels 192; Gaps 26;

QY 95 PTLNDFSHLYRSEYRIRAIQHEGSEAFSGRYKLG----FTRSAGITREMA 150
 DB 107 PKLTDF-----DLHVFEGNHHRIYEKLGALMTVDGKGVFAVWA 148
 QY 151 PGASHALVGDENNPNADTWRDDYGVWFELP-----NNADG--SPAIP 195
 DB 149 PNANVSLDGPNNMDGLHQKRNKNVWELFELGVGTGYKYEIKWBGHIYEKTD 208
 QY 196 HGRVKRIMDTPSGYKDISAMIKSVQAPGEIPENGIIYDPEEKKYFQHPQRPBS 255
 DB 209 YGFQGVAPKTAIYAD-----LDG--YQWHDDEWLKARTSDLSKRP 249
 QY 256 LRIYESHIG---MSPEP-----KINSYANFDEVLPRIKLGY 291
 DB 250 VSVYELHIGSLHTYVDEPVKTLHGEGVVEVSEWNTARFLTYVLDCLAYVELGY 309
 QY 292 NAVQIMAIQESHYVAFGYHTVNFAPSRFGTPEDLSKLDPAHELGILVMDIVHSHS 351
 DB 310 THIELPLFAHEHFDPSGWGYVAFTRFGSPEDPMKFFVDCCHNGICVILDWYVGHF 369
 QY 352 SNNLTLDGNGPDGDTYHYFGGR-GHHMMDSRLFNYSGEVYLRLLSNARWMBEYK 410
 DB 370 PKDG-HGLAFPDGTHL-YEHGDPKKEGHEKWTLLINYSGEVRFNPLVANALFMPKXTH 427
 QY 411 DGFREDGTVSMYTHGLQMTFTGNVGEY---FGFATVDVAVYMLVNDLHGLHPDA 466
 DB 428 DGMRVDAVASMVY-----LDYCREGGEVANEYGERENLEADFLQVNVSVYTFPGI 481
 QY 467 VSIGEDVSGMPTECLVPDGVGVFDYRLMA-----VADKWEILLQSDSESWMGD 517
 DB 482 LSTAEESTWPMVSWMTYVGGIGFNKKMMGNHMDLMDYSDMPWRQFQNSITFSM-- 539
 QY 518 IVHTLTNRRLKCVTY--AESHDALVGDXTAFMLMDKMDTDFNALDPSPIRIDGI 575
 DB 540 -----WYNHSENYMLALSHDEVVHG-KSNMLGKMPDEWQKXANVR----- 579
 QY 576 ALHKMIRLVTMGIGSGYLN-FWNGEFGH-PEW-----IDPRGQTLPTGKLP 623
 DB 580 -----ALPTYNFTHPGKTKTMSMEFGQSENNWMDLEWHLINFPHQD----- 624
 QY 624 GNNNSYDKRRRRLDGLADFLRYHGMQEPDQAMQHLSE-----KYGFMTEHQYVSRKA 677
 DB 625 -----LKQFTELNHTLYKNRPALYSNDFDSGGFWIDCSD 659

QY 678 ESDKTIIFERGD-----LVFVFNFMNSFFDYRVCGRPKYKVALDSDDALFGGRSR 731
 DB 660 NHHSVSFFRRKAKNSAEFVYITNCF--TPQPHSHYRQVVPYPCGFTELFNSGARQYGG-SN 717

QY 732 LDHVDYFTTEHFDNRPRSFVYTPSRFAVYALTE 768
 DB 718 MGNLGKMTSEWSFHQPYSLDCLPPLSVLYKLKLSQ 754

RESULT 14
 GLOB_OCEIH STANDARD; PRT; 637 AA.
 AC 08C2E8;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
 enzyme) (B3) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-
 transferase).
 GN GLGB OR OB0406.
 OS Oceanobacillus iheyensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
 OX NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HTE81 / DSM 14371 / JCM 11309;
 RX MEDLINE=2220767; Pubmed=2235376;
 RA Takami H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 CC - FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
 CC linkages in glycogen by scission of a 1,4-alpha-linked
 CC oligosaccharide from growing alpha-1,4-glucan chains and the
 CC subsequent attachment of the oligosaccharide to the alpha-1,6
 CC position (By similarity).
 CC - CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
 CC glycogen.
 CC - PATHWAY: Glycogen biosynthesis; third step.
 CC - SUBUNIT: Monomer (By similarity).
 CC - SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 CC or send an email to license@isb-sib.ch).

CC EMBL: AP004584; BAC12362.1; --
 CC HAMAP: MF_00685; --; 1.
 CC InterPro: IPR006589; Alp_amy1_cat_sub.
 CC InterPro: IPR006047; Alp_amy1_cat.
 CC InterPro: IPR006407; GlbB.
 CC InterPro: IPR004193; Glyco_hydro_13N.
 CC Pfam: PF00128; alpha-amyase; 1.
 CC Pfam: PF02922; Isoamylase; 1.
 CC SMART: SM00642; Amy; 1.
 CC TRFPMs: TIGR01515; branching_enzym; 1.
 CC Glycogen biosynthesis; Transferrase; Glycosyltransferase;
 CC Complete proteome.
 CC ACT_SITE 202 BY SIMILARITY.
 CC ACT_SITE 237 BY SIMILARITY.
 CC ACT_SITE 242 BY SIMILARITY.
 CC ACT_SITE 305 BY SIMILARITY.
 CC ACT_SITE 307 BY SIMILARITY.
 CC ACT_SITE 361 BY SIMILARITY.
 CC ACT_SITE 428 BY SIMILARITY.
 CC ACT_SITE 429 BY SIMILARITY.
 CC SEQUENCE 637 AA; 74651 MW; 2A5165A2556A269D CRC64;

Query Match 13.7%; Score 571.5; DB 1; Length 637;
 Best Local Similarity 25.9%; Pred. No. 2e-34;
 Matches 173; Conservative 103; Mismatches 239; Indels 153; Gaps 26;

QY 139 RAAGETTYEMAPGASALVDPENNNPNADMTM- DDYGVWIEFLPNNADSGPAIPHG 197
 DB 32 KKKRGYRFAVWAPNALKVCVGDFFNNMEESHLEKRTDGLWGCFI---ADIPPAISYK 88
 QY 198 SHVKIMDTPSGVSKDSISAWIKESVQAPGEIPENGIV-----YDPPEEKYV 244
 DB 89 YHICSEDDISLKADPPATQAEERPKASVIRPANGQWSDQWIEQRNTYD----- 141
 QY 245 FQHPOKRPESLRIYSHIG--MSPEPKINSYANPDEVLPRIKLGYNAVOIMAIQEH 302
 DB 142 YSSP-----ISIEVHLGTWKKTKKQFLSYRELATOLIPYKSGYTHIELLPINEH 194
 QY 303 SYVASGCHVTNFAFSSRGTPEDEKSLIDRAHELGILVIMDIYHSHSSNNTLGINGF 362
 DB 195 PDRSRWGQYIGTGFVAVTSRYGNPSDFKYFDQHQHOGIVLDWPGHFCXDDF--GLRQF 253
 QY 363 DQTDITFPGGPRGHMMMDSRLEFNYSWVLEPFLSNAMWLEEKYFDPGFRPGVTSM 422
 DB 254 DQAPLYEYDPRKSEKSKWGTLAFDYGRPVQSLINATYWLKEPHIDGLRVDVAVSM 313
 QY 423 YTHHGLQMTFTNGYGEY-----FGPATVDVAVYLMVNDLHGHPDAVISGEDV 473
 DB 314 YL-----NFDRYDEEEKTYNTYTGGEENLEAFALRLKLNKVFPSYIPGALMAEDS 363
 QY 474 SGMPTECIPVDPDGVGDYELHMAVADKW--ELIKQDESCKMGDIYHTLNRBW----- 527
 DB 364 SOLPLVTAPARKKGLGNYKWNNG---WMDLL-----SMEKESGTH---RKHNNRL 410
 QY 528 -LEKCVTAE-----SHDQALVGDKTIAFWLMDK---DMYDFVALDRPSTPRIDRGIAL 577
 DB 411 TSPFWTYEENYLLPLSHDEVHAGKS---LDDKMGGDQWQQA----- 451
 QY 578 HKMIRLVTMGLGEGY-----LNMGNBFG--HPMWIDFPRGPQL--PTGKVLFGN 625
 DB 452 -NLRL-----YGVYVTHPCKKLIVMGELAQYAEWKQTEELDMHLEBPLKGI--- 500
 QY 626 NNSYDKCRRRFDGDDFLAYHGMQGEEDQAMQHLEKY--GFMTSEHQYVSRKHEEDVI 683
 DB 501 -----YHYIKNINELYQHPLEIYELDHLSEGEFWIDPHRIDQSVI 540
 QY 684 IFEER-----GDIVFVNFHMSNFPDYRVGCSRPRKYKVALDSDDDLFGGFSRLDHVD 737
 DB 541 ARRRKANKRQBELIITCNF--TPQVHFDYKIGVPSGKKEIFNDSVRFSSGQINSEGH 599
 QY 738 YETTEHPH 745
 DB 600 FSPPEKMH 607

RESULT 15

GLGB_COREF STANDARD; PRT; 731 AA.
 ID GLGB_COREF
 AC 08FO12;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-transferase).
 DE GN GLGB OR C61323.
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 OC NCB1 TaxID=152794;
 OX NCB1
 RN
 RP SEQUENCE FROM N.A.
 RP STRAIN=VS-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RX MEDLINE=22723752; PubMed=12840036;

RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
 RA Sugimoto S., Matsui K., Yamagishi A., Kinuchi H., Ikeo K.,
 RA Gojobori T.,
 RT "Comparative complete genome sequence analysis of the amino acid
 RT replacements responsible for the thermostability of Corynebacterium
 RT efficiens";
 RU Genome Res. 13:1572-1579 (2003).
 CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
 CC linkages in glycogen by scission of a 1,4-alpha-linked
 CC oligosaccharide from growing alpha-1,4-glucan chains and the
 CC subsequent attachment of the oligosaccharide to the alpha-1,6
 CC position (By similarity).
 CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
 CC glycogen.
 CC -1- PATHWAY: Glycogen biosynthesis; third step.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC or send an email to license@sib.ch).

CC EMBL: AP005218; BAC18133.1; -.
 DR HAMAP: MF_00685; -; 1.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alpba_amy1_cat.
 DR InterPro: IPR006407; GLGB.
 DR InterPro: IPR004193; Glyco_hydro_13N.
 DR Pfam: PF00128; alpha-amy1ase; 1.
 DR Pfam: PF02922; isoamy1ase_N; 1.
 DR SMART: SM00642; Amyy; 1.
 DR TIGRFAMs: TIGR01515; branching enzym; 1.
 DR Glycogen biosynthesis; transferase; Glycosyltransferase;
 KM Complete proteome.
 FT ACT_SITE 303 BY SIMILARITY.
 FT ACT_SITE 303 BY SIMILARITY.
 FT ACT_SITE 338 BY SIMILARITY.
 FT ACT_SITE 343 BY SIMILARITY.
 FT ACT_SITE 406 BY SIMILARITY.
 FT ACT_SITE 408 BY SIMILARITY.
 FT ACT_SITE 461 BY SIMILARITY.
 FT ACT_SITE 528 BY SIMILARITY.
 FT ACT_SITE 529 BY SIMILARITY.
 SQ SEQUENCE 731 AA; 82714 MW; 63B5690B96EDB4E CRC64;

Query Match 13.6%; Score 568.5; DB 1; Length 731;
 Best Local Similarity 26.4%; Pred. No. 4.1e-34;
 Matches 196; Conservative 124; Mismatches 264; Indels 159; Gaps 34;

QY 75 GEKPRVVPKPGDQKIYEIDPTLKDFRSHLDVRSYERIRAIIDQHE---GGLEAFSRG 131
 DB 91 GQDPVYVADP-----YIFLPLTGEMDYTL---ISGR-----HERIMVDLGANVKT 133
 QY 132 YE-KLGFTRSAEGITYREMAFGASALVDPENNNPNADTM--TRDDYGVWIEFLPNNAD 189
 DB 134 YETTLGQYR---GTFAPVAPNALGAVLIGFNGMNASQHAMSLGSGGIWELFIPN--- 187
 QY 190 GSPALPHGSRKYLIMDTPSG-VKDSISAWIKESVQAP--GEIFPNGIYVDPPEEKVFPQ 246
 DB 188 ---IGPEVVEYKFAIQTRSGHRDKADPMARLAELRPAGTSIV-----ESDQWQ 234
 QY 247 HPO--PKRPE-----SLRIYESHIGMSSPEPKINSYANFDEVLPRIKLGYNAVOIMA 298
 DB 235 DSEWMDKAEIDTATTPMSVYEVHLSGWRG---RYALATATLVVDVADLGTTHVEFWP 291
 QY 299 IQEHSYVAFGYHVTNFFAPSSRFGTPEDKSLIDRAHELGILVMDIYHSHSSNNTLDG 358
 DB 292 VAEHPFGSGWGYOVGYAPTSRWGSPDELRLKLDLFAHAGIGVILIDWVPAHPKDW-A 350
 QY 359 LMGFDGTTHYHGSRGHHMMWMDSRLEFNYSWVLEPFLSNAMWLEEKYFDPGFRPDGV 418


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Db 351 LARFDQALYEHDPWRGGEQKDWGTYFNGRSEVNFVANNALYMLSEFHVDELRYDAV 410
QY 419 TSMYTHHGLQMTFTGNYGEY---FGFATVDVAVYIYMLVNDLIHGLHPDAVSIGEDVS 474
Db 411 ASMLY-----LDSRHGEMERPVYGRNLEAVCFLOENNAIVQVRHPGALITAEEST 464
QY 475 GMPTFCIPYDGGVGEDYRLMAVADKMIELKOSDSWKMGDIYHTLTNRMLKCYTY 534
Db 465 SWPGVTAPRTWDGGIGFSLKNNMGWMDLTLEYFSK-----DPIHRSFHHNELTFSLVY 516
QY 535 A-----ESHQALVGDKTIAFWLMDKMYDPMALDRPSTPRIDRGIALHKMIRLVTM 586
Db 517 AFSERFVLPISHDELVHKGSL-W-----NRMFGDTWKKAGMRTILAYYMA 562
QY 587 GLGGEYLNFMGNEFG-HPEWIDFPRGPQTLPTGKVLPGNNNSYDKCRRRFDLGDADFLR 645
Db 563 HPQKK-LLEMGEITGQDEWSE---AHELPMG-VVEGMOGEYHE-----GISDLVR 608
QY 646 YHGMQEFDAQWQHLBEKYGFTSEHQ-----YVSRQHEE--DKVITPER-GD---LV 691
Db 609 -----ELNSTYKEVTALHQDFSGEGFTWNRKADDAANNILVFTRRHGDGSOQL 656
QY 692 FVFRFHMNSFPDYRVGSRPGKXKVALDSDDALFGFS-----RLDHDVDFYFTT 741
Db 657 CVFNLS-GTSQPEYQIGVSGGSWRLVLTNDEQYHGANNPLPETTEAKIDRDGFPYTT 715
QY 742 EHPHNRPRSFVYTPSRRAVY 764
Db 716 -----TMSPMASQFY 727
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Search completed: April 15, 2004, 08:37:03
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: April 15, 2004, 08:35:16 ; Search time 52 Seconds
(without alignment)
4659.361 Million cell updates/sec

Title: US-09-508-377-12
Perfect score: 4169
Sequence: 1 MATFAVSGATLVARPPAA.....PRFSVTPSTRAVVALTE 768

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4169	100.0	768	10 Q9ATB5	Q9ATB5 triticum ae
2	4119.5	98.8	823	10 Q9ATU7	Q9ATU7 triticum ae
3	4113.5	98.7	823	10 P93691	P93691 triticum ae
4	4049.5	97.1	819	10 Q9ATB6	Q9ATB6 aegilops ta
5	3937	94.4	734	10 Q9ATB7	Q9ATB7 hordeum vul
6	3915	93.9	729	10 Q24397	Q24397 triticum ae
7	3685	88.4	841	10 Q96X19	Q96X19 oryza sativ
8	3588.5	86.1	814	10 Q24421	Q24421 zea mays (m
9	3362	80.6	825	10 Q40663	Q40663 oryza sativ
10	3351.5	80.4	833	10 Q7XZK7	Q7XZK7 sorghum bic
11	3351	80.4	799	10 Q81387	Q81387 zea mays (m
12	3348.5	80.3	829	10 Q9ZTB6	Q9ZTB6 hordeum vul
13	3346	80.3	922	10 Q41058	Q41058 pisum sativ
14	3307.5	79.3	870	10 Q9XIS5	Q9XIS5 phaseolus v
15	3258	78.1	800	10 Q42531	Q42531 arabidopsis
16	3258	78.1	805	10 Q9L2S3	Q9L2S3 arabidopsis

17	3257.5	78.1	868	10 Q948N7	Q948N7 ipomoea bat
18	3219	77.2	696	10 Q9ATV7	Q9ATV7 ipomoea bat
19	3207	76.9	830	10 Q49953	Q49953 solanum tub
20	3194	76.6	836	10 Q9XGA7	Q9XGA7 solanum tub
21	3192	76.6	871	10 Q9XGA5	Q9XGA5 solanum tub
22	3180	76.3	878	10 Q9XGA6	Q9XGA6 solanum tub
23	3155	75.7	858	10 Q23647	Q23647 arabidopsis
24	3135	75.2	854	10 Q42526	Q42526 arabidopsis
25	3135	75.2	882	10 Q9XGA8	Q9XGA8 solanum tub
26	2193.5	52.6	830	10 Q04074	Q04074 triticum ae
27	2189.5	52.5	775	10 Q7XZK6	Q7XZK6 hordeum vul
28	2187	52.5	852	10 Q08131	Q08131 manihot esc
29	2175.5	52.2	833	10 Q9FTU8	Q9FTU8 triticum ae
30	2173.5	52.1	810	10 Q9XGB3	Q9XGB3 triticum ae
31	2173.5	52.1	833	10 Q9XGB1	Q9XGB1 triticum ae
32	2173.5	52.1	865	10 Q9XGB2	Q9XGB2 triticum ae
33	2172.5	52.1	847	10 Q9XIS4	Q9XIS4 phaseolus v
34	2168.5	52.0	830	10 Q04864	Q04864 solanum tub
35	2166.5	52.0	820	10 Q40664	Q40664 oryza sativ
36	2161.5	51.8	820	10 Q7XZP9	Q7XZP9 oryza sativ
37	2156	51.7	832	10 Q9XGP8	Q9XGP8 sorghum bic
38	2146	51.5	823	10 Q41740	Q41740 zea mays (m
39	2138	51.3	823	10 Q84XW7	Q84XW7 zea mays (m
40	2136	51.2	702	4 Q96ENO	Q96ENO homo sapien
41	2134.5	51.2	807	10 Q9XED2	Q9XED2 triticum ae
42	2127	51.0	702	11 Q9D6T9	Q9D6T9 mus musculu
43	2099.5	50.4	826	10 Q41059	Q41059 pisum sativ
44	2059	49.4	689	3 Q96VA4	Q96VA4 aspergillus
45	2049	49.1	686	3 Q9Y8H3	Q9Y8H3 emericella

ALIGNMENTS

Query	1	PRELIMINARY:	PRT:	768 AA.
Q9ATB5	Q9ATB5			
AC	Q9ATB5			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Starch branching enzyme IIA variant.			
OS	Triticum aestivum (wheat).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;			
OC	Triticeae; Triticum.			
OX	NCBI_TaxID=4565;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
FX	MEDLINE=21140316; PubMed=11244112;			
RA	Abraham S., Regina A., Li Z., Mukal Y., Yamamoto M., Kosar-Hashemi B.,			
RA	Abraham S., Morell M.K.,			
RT	"Comparison of Starch-Branching Enzyme Genes Reveals Evolutionary			
RT	Relationships Among Isoforms. Characterization of a Gene for Starch-			
RT	Branching Enzyme IIA from the wheat D Genome Donor Aegilops			
RT	tauschii."			
RL	Plant Physiol. 125:1314-1324 (2001).			
DR	EMBL; AF384332; AAK26822.1; "			
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.			
DR	GO; GO:0004553; F:hydrolyase activity; hydrolyzing O-glycosyl . . . ; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha-amyl_cat.			
DR	InterPro; IPR004193; Glyco_hydro_13N.			
DR	InterPro; IPR007110; IG-like.			
DR	Pfam; PF00128; alpha-amylase; 1.			
DR	Pfam; PF02922; isoamylase N; 1.			
DR	SEQUENCE 768 AA; 87430 MW; E084037755084A8F CRC64;			
SQ				
Query Match	100.0%; Score 4169; DB 10;			
Best Local Similarity	100.0%; Pred. No. 2e-303;			
Matches 768; Conservative 0;	Mismatches 0;			
Indels 0;	Gaps 0;			
1 MATFAVSGATLVARPPAAQPEELQIPEDIEBQTAENVMTGCTAETLESSEPTGIVET 60				

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Db      1 MATFAVSATLGVARRPAAQPELQIPEDIEQTAENVNTGTAELKESSEPTQGIIVET 60
QY      61 IIDGVTGKVELVGEKPRVYVPRGQDQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQ 120
Db      61 IIDGVTGKVELVGEKPRVYVPRGQDQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQ 120
QY      121 HEGGLEAFSRGYEKLGFTRSAEGITTYEWAPGAHSALVGDENNANADMTDIDYGVW 180
Db      121 HEGGLEAFSRGYEKLGFTRSAEGITTYEWAPGAHSALVGDENNANADMTDIDYGVW 180
QY      181 EITFLPNNAGSPALPHGSRVKIRMDTPSGVSDISAMIKFSVQAPGELPENGIIYDPEE 240
Db      181 EITFLPNNAGSPALPHGSRVKIRMDTPSGVSDISAMIKFSVQAPGELPENGIIYDPEE 240
QY      241 EKVFPQHPQKPEBSLRIVESHIGMSSPEPKINSYANFRDEVLPRIKELGYNAVQIMAIQ 300
Db      241 EKVFPQHPQKPEBSLRIVESHIGMSSPEPKINSYANFRDEVLPRIKELGYNAVQIMAIQ 300
QY      301 EHSYVASFYHVTNFPAPSSRFCTPEDLKSILIDRAHELGLVLMIDYHSHSNNTLDGLN 360
Db      301 EHSYVASFYHVTNFPAPSSRFCTPEDLKSILIDRAHELGLVLMIDYHSHSNNTLDGLN 360
QY      361 GPDGTTTHYHGGPRGHHMMWDSLENYGSEVLRFLISNARWMLBEEKFDFGFPDGYTS 420
Db      361 GPDGTTTHYHGGPRGHHMMWDSLENYGSEVLRFLISNARWMLBEEKFDFGFPDGYTS 420
QY      421 NMVTHGLQMTFTGNVGEYFGFATDVAVVYLMVNDLIHGLHPDAYSIGEDVSGMPTFC 480
Db      421 NMVTHGLQMTFTGNVGEYFGFATDVAVVYLMVNDLIHGLHPDAYSIGEDVSGMPTFC 480
QY      481 IVPDGGVGFDFRILHMAVADKMIELKQSDSWKMGDIVHTLTNRWLEKCVTYAESHDQ 540
Db      481 IVPDGGVGFDFRILHMAVADKMIELKQSDSWKMGDIVHTLTNRWLEKCVTYAESHDQ 540
QY      541 ALVGDKTIAWMDKMDYDPMALDRPSTPRIDRGIALHKMRLVTMGSGGYLNFMGNE 600
Db      541 ALVGDKTIAWMDKMDYDPMALDRPSTPRIDRGIALHKMRLVTMGSGGYLNFMGNE 600
QY      601 FGHPEWIDFPRGPOTLPFGKYLPGNNNSYDKCRRRFDLGADFLRYHGMQEPDQMOHLE 660
Db      601 FGHPEWIDFPRGPOTLPFGKYLPGNNNSYDKCRRRFDLGADFLRYHGMQEPDQMOHLE 660
QY      661 EKYGFMTSEHQYVSRKHEDEKYLIFERGDIVFVFNFMHNSFFDYRVGCSRGKYKVALD 720
Db      661 EKYGFMTSEHQYVSRKHEDEKYLIFERGDIVFVFNFMHNSFFDYRVGCSRGKYKVALD 720
QY      721 SDDALFGFSRLDHDVDVFTTEHPHDNRPRSFSVYTPSRITAVVYALTE 768
Db      721 SDDALFGFSRLDHDVDVFTTEHPHDNRPRSFSVYTPSRITAVVYALTE 768

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RESULT 2

Q9FUU7 PRELIMINARY; PRT; 823 AA.

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ID Q9FUU7 AC Q9FUU7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Search branching enzyme 2 (EC 2.4.1.81).
GN SBE2.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticaceae; Triticum.
OC Triticaceae; Triticum.
OC NCBI_Taxid=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Cheyenne, TISSUE=Endosperm;
RA McCue K.F., Harkman W.J., Tanaka C.K., Anderson O.D.;
RT "Search Branching Enzymes Sbe1 and Sbe2 from Wheat (Triticum aestivum
RT cv. Cheyenne): Molecular Characterization, Developmental Expression,
and Homolog Assignment by Differential PCR.";

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BL Submitted (JUL-2000) to the EMBL/Genbank/DDBJ databases.
DR EMBL; AF286319; AAC27623.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0004553; F:hydrolyase activity; hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha.amyl cat.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02922; isoamylase N; 1.
KW Glycosyltransferase; Transferase.
SQ
SEQUENCE 823 AA; 92970 MW; 58915B0B65A462A CRC64;

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Query Match 98.8%; Score 4119.5; DB 10; Length 823;
Best Local Similarity 93.1%; Pred. No. 12e-299;
Matches 766; Conservative 0; Mismatches 2; Indels 55; Gaps 1;

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QY      1 MATFAVSATLGVARRPAAQPELQIPEDIEQTAENVNTGTAELKESSEPTQGIIVET 19
Db      1 MATFAVSATLGVARRPAAQPELQIPEDIEQTAENVNTGTAELKESSEPTQGIIVET 19
QY      20 -----AQPFLQIPEDIEQTAENVNTGTAELKESSEPTQGIIVETIDGV 65
Db      20 -----AQPFLQIPEDIEQTAENVNTGTAELKESSEPTQGIIVETIDGV 65
QY      61 VLPDGSDDLASPAQPELQIPEDIEQTAENVNTGTAELKESSEPTQGIIVETIDGV 120
Db      61 VLPDGSDDLASPAQPELQIPEDIEQTAENVNTGTAELKESSEPTQGIIVETIDGV 120
QY      66 TKGVLELVGEKPRVYVPRGQDQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQHEGGL 125
Db      66 TKGVLELVGEKPRVYVPRGQDQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQHEGGL 125
QY      121 TKGVLELVGEKPRVYVPRGQDQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQHEGGL 180
Db      121 TKGVLELVGEKPRVYVPRGQDQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQHEGGL 180
QY      181 EAFSRGYEKLGFTRSAEGITTYEWAPGAHSALVGDENNANADMTDIDYGVWIFLP 185
Db      181 EAFSRGYEKLGFTRSAEGITTYEWAPGAHSALVGDENNANADMTDIDYGVWIFLP 185
QY      241 NNADSPALPHGSRVKIRMDTPSGVSDISAMIKFSVQAPGELPENGIIYDPEE 245
Db      241 NNADSPALPHGSRVKIRMDTPSGVSDISAMIKFSVQAPGELPENGIIYDPEE 245
QY      301 QHPQRPESLRIVESHIGMSSPEPKINSYANFRDEVLPRIKELGYNAVQIMAIQESHY 305
Db      301 QHPQRPESLRIVESHIGMSSPEPKINSYANFRDEVLPRIKELGYNAVQIMAIQESHY 305
QY      361 ASFGYHVTNFPAPSSRFCTPEDLKSILIDRAHELGLVLMIDYHSHSNNTLDGLNGFDG 365
Db      361 ASFGYHVTNFPAPSSRFCTPEDLKSILIDRAHELGLVLMIDYHSHSNNTLDGLNGFDG 365
QY      421 DTHYFHGPRGHHMMWDSLENYGSEVLRFLISNARWMLBEEKFDFGFPDGYTSMTYTH 425
Db      421 DTHYFHGPRGHHMMWDSLENYGSEVLRFLISNARWMLBEEKFDFGFPDGYTSMTYTH 425
QY      481 HGLQMTFTGNVGEYFGFATDVAVVYLMVNDLIHGLHPDAYSIGEDVSGMPTFCIPVD 485
Db      481 HGLQMTFTGNVGEYFGFATDVAVVYLMVNDLIHGLHPDAYSIGEDVSGMPTFCIPVD 485
QY      541 GGVGFDYRLHMAVADKMIELKQSDSWKMGDIVHTLTNRWLEKCVTYAESHDQALVGD 545
Db      541 GGVGFDYRLHMAVADKMIELKQSDSWKMGDIVHTLTNRWLEKCVTYAESHDQALVGD 545
QY      601 KTIAPWMDKMDYDPMALDRPSTPRIDRGIALHKMRLVTMGSGGYLNFMGNEFGHPE 605
Db      601 KTIAPWMDKMDYDPMALDRPSTPRIDRGIALHKMRLVTMGSGGYLNFMGNEFGHPE 605
QY      666 WIDFPRGPOTLPFGKYLPGNNNSYDKCRRRFDLGADFLRYHGMQEPDQMOHLEEKYGF 665
Db      666 WIDFPRGPOTLPFGKYLPGNNNSYDKCRRRFDLGADFLRYHGMQEPDQMOHLEEKYGF 665
QY      721 MTSEHQYVSRKHEDEKYLIFERGDIVFVFNFMHNSFFDYRVGCSRGKYKVALDSDAL 780
Db      721 MTSEHQYVSRKHEDEKYLIFERGDIVFVFNFMHNSFFDYRVGCSRGKYKVALDSDAL 780
QY      726 FGFPSRLDHDVDVFTTEHPHDNRPRSFSVYTPSRITAVVYALTE 768
Db      726 FGFPSRLDHDVDVFTTEHPHDNRPRSFSVYTPSRITAVVYALTE 768
QY      781 FGFPSRLDHDVDVFTTEHPHDNRPRSFSVYTPSRITAVVYALTE 823
Db      781 FGFPSRLDHDVDVFTTEHPHDNRPRSFSVYTPSRITAVVYALTE 823

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RESULT 3
P93691 PRELIMINARY; PRT; 823 AA.
ID P93691
AC P93691;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE 1,4-alpha-glucan branching enzyme II precursor (EC 2.4.1.18).
GN SBE2.
OC Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OC NCBI_taxid=4565;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Fielder;
RA Nair R.B., Baga M., Scoles G.J., Kartha K.K., Chibbar R.N.;
RT "Isolation, characterization and expression analysis of a starch
branching enzyme II cDNA from wheat.";
RL Plant Sci. 0:0-0(0).
DR EMBL; Y11282; CAA72154.1; .
DR PIR; T06574; T06574.
DR GO; GO:0003844; F.1.4-alpha-glucan branching enzyme activity; IEA.
DR GO; GO:0004556; F.alpha-amylose activity; IEA.
DR GO; GO:0004553; F.hydrolase activity, hydrolyzing O-glycosyl. . .; IEA.
DR GO; GO:0016757; F.transfructose activity, transferring glycosyl. . .; IEA.
DR GO; GO:0005975; P.carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR InterPro; IPR007110; Ig-1like.
DR Pfam; PF00128; alpha-amylose; 1.
DR Pfam; PF02922; isoamylase N; 1.
DR GlycoStyl; glycosyltransferase; Signal; Transferase.
FT SIGNAL 1 54 POTENTIAL.
FT CHAIN 55 823 1,4-ALPHA-GLUCAN BRANCHING ENZYME II.
SQ SEQUENCE 823 AA; 92936 MW; 80135FA52CBA4549 CRC64;

Query Match 98.7%; Score 4113.5; DB 10; Length 823;
Best Local Similarity 93.0%; Pred. No. 3.3e-299;
Matches 765; Conservative 0; Mismatches 3; Indels 55; Gaps 1;

QY 1 MATFAVSGATLGVARPPAA----- 19
DB 1 MATFAVSGATLGVARPPAGAGGGLPRSGSRRGGVDDPSLLRKDSSRAVLSRAAPGK 60
QY 20 -----AOEELQIPEDIEQTAEVNMTGTAELKESSEPTQIVETITDGV 65
DB 61 VLVPPGESDLDLAPAPQEEIQTIEDIEQTAEVNMTGTAELKESSEPTQIVETITDGV 120
QY 66 TGVKVELVVEGKRPVYKPKDGOKIYEDPTLKDFRSHLDVRYSEYRIRAIIDQHEGGL 125
DB 121 TGVKVELVVEGKRPVYKPKDGOKIYEDPTLKDFRSHLDVRYSEYRIRAIIDQHEGGL 180
QY 126 EAFSRGVEKLGFRSAAGITTYRENAFAHSAALVGDNNMNPNDTMTTRDYGWEIFLP 185
DB 181 EAFSRGVEKLGFRSAAGITTYRENAFAHSAALVGDNNMNPNDTMTTRDYGWEIFLP 240
QY 186 NNADGSPALPHGSRVYKRMTPSGVKDSISAMIKFSVOAPEIFPNCIYVDPPEEKVVF 245
DB 241 NNADGSPALPHGSRVYKRMTPSGVKDSISAMIKFSVOAPEIFPNCIYVDPPEEKVVF 300
QY 246 QHPQKRPESLRIVESHIGSSPEPKINSYANFRDEVLPRIKRLGYNAVOIMAIQESHY 305
DB 301 QHPQKRPESLRIVESHIGSSPEPKINSYANFRDEVLPRIKRLGYNAVOIMAIQESHY 360
QY 306 ASFGYHTNFAASSRGTGEDDKSLIDRAHEGLLVLMIDVHSHSNNTLDGLNGPCT 365
DB 361 ASFGYHTNFAASSRGTGEDDKSLIDRAHEGLLVLMIDVHSHSNNTLDGLNGPCT 420
QY 366 DTHYFHGPRGHHMMWDSRLFNYSGWVLRFLSNARWMLLEEKYFDGPRFGVTSMMYTH 425

DB 421 DTHYFHGPRGHHMMWDSRLFNYSGWVLRFLSNARWMLLEEKYFDGPRFGVTSMMYTH 480
QY 426 HGLQMTFTGNNGEYGFATDVAVVYLMVNLILHGLHDAVSIQDVSGMPTFCIPVD 485
DB 481 HGLQMTFTGNNGEYGFATDVAVVYLMVNLILHGLHDAVSIQDVSGMPTFCIPVD 540
QY 486 GGVGFYDYLHNAVADKWIIEELKQSDSWKMGDIIVHTLNNRMLEKCVTAESHDAQLVGD 545
DB 541 GGVGFYDYLHNAVADKWIIEELKQSDSWKMGDIIVHTLNNRMLEKCVTAESHDAQLVGD 600
QY 546 KTIAPWMDKMDYDPMALDPRSTPRIDGIALHKRIYTMGIGRGYLNFMNGEFAPE 605
DB 601 KTIAPWMDKMDYDPMALDPRSTPRIDGIALHKRIYTMGIGRGYLNFMNGEFAPE 660
QY 606 WIDFPRGQTLPTGKVLPGNNNSYDKCRRRFDLGDADFLRYHGMQEPDAMHLEEKYGF 665
DB 661 WIDFPRGQTLPTGKVLPGNNNSYDKCRRRFDLGDADFLRYHGMQEPDAMHLEEKYGF 720
QY 666 MTSEHQYVSRKHEDEKVIIFERGDVFEVNFHWSNFPDYRVGCSRPGRYKVALDSDDAL 725
DB 721 MTSEHQYVSRKHEDEKVIIFERGDVFEVNFHWSNFPDYRVGCSRPGRYKVALDSDDAL 780
QY 726 FGGFRLDHDVDVFTTEHPHNDPRPSFSYVTSRTAVVYALTE 768
DB 781 FGGFRLDHDVDVFTTEHPHNDPRPSFSYVTSRTAVVYALTE 823

RESULT 4
Q9ATB6 PRELIMINARY; PRT; 819 AA.
ID Q9ATB6
AC Q9ATB6;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Starch branching enzyme IIa.
OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Aegilops.
OC NCBI_taxid=37682;
[1]
RN
RP SEQUENCE FROM N.A.
RC MEDLINE=21140316; PubMed=11244112;
RA Rahman S., Regina A., Li Z., Mukai Y., Yamamoto M., Kosar-Hashemi B.,
Abraham S., Korell M.K.;
RT "Comparison of Starch-Branching Enzyme Genes Reveals Evolutionary
Relationships Among Isoforms. Characterization of a Gene for Starch-
Branching Enzyme IIa from the wheat D Genome Donor Aegilops
tauschii.";
RT Plant Physiol. 125:1314-1324(2001).
DR EMBL; AP38431; AA26821.1; .
DR GO; GO:0004556; F.alpha-amylose activity; IEA.
DR GO; GO:0004553; F.hydrolase activity, hydrolyzing O-glycosyl. . .; IEA.
DR GO; GO:0005975; P.carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR InterPro; IPR007110; Ig-1like.
DR Pfam; PF00128; alpha-amylose; 1.
DR Pfam; PF02922; isoamylase N; 1.
SQ SEQUENCE 819 AA; 92607 MW; E41F63050E501AA4 CRC64;

Query Match 97.1%; Score 4049.5; DB 10; Length 819;
Best Local Similarity 92.1%; Pred. No. 2e-294;
Matches 754; Conservative 6; Mismatches 8; Indels 51; Gaps 1;

QY 1 MATFAVSGATLGVARPPAA----- 16
DB 1 MATFAVSGATLGVARPPAGAGGGLPRSGSRRGGVDDPSLLRKDSSRAVLSRAAPGKVLVP 60
QY 17 -----PAAAPPEIQTIEDIEQTAEVNMTGTAELKESSEPTQIVETITDGVTKGV 69
DB 61 DDESDDLAPAPQEEIQTIEDIEQTAEVNMTGTAELKESSEPTQIVETITDGVTKGV 120

QY 70 KEIVGSEKPRVVPKPDGQKIYEIDPLKDFRSHLDYRYSRRIIRAIDHEGGLNFS 129
 DB 121 KEIVGSEKPRVVPKPDGQKIYEIDPLKDFRSHLDYRYSRRIIRAIDHEGGLNFS 180
 QY 130 RGVEXKGFRTSAGITITREWAPGASHALYVDFNNMNPADITMRDVGWEIPLNNAD 189
 DB 181 RGVEXKGFRTSAGITITREWAPGASHALYVDFNNMNPADITMRDVGWEIPLNNAD 240
 QY 190 GSPALPHGSRVKIRMDTPSGVKOSISAMIKFSVQAPGEIPNGIYDPEEKKYVQHPQ 249
 DB 241 GSPALPHGSRVKIRMDTPSGVKOSISAMIKFSVQAPGEIPNGIYDPEEKKYVQHPQ 300
 QY 250 PKRPESLRIYESHIGMSPEPKINSYANFDEVLPRIKRGYNAVQIALQESHYASFG 309
 DB 301 PKRPESLRIYESHIGMSPEPKINSYANFDEVLPRIKRGYNAVQIALQESHYASFG 360
 QY 310 YHVTNFPAPSSRGTPEDLSLIDRAHELGLVMDIVSHSSNNITDGLNGFGDTTHY 369
 DB 361 YHVTNFPAPSSRGTPEDLSLIDRAHELGLVMDIVSHSSNNITDGLNGFGDTTHY 420
 QY 370 FHGPRGHMMWMDSRLEFNYSWEVLRFLSNARWLEBYKDFRPGDVTSMYTHGLQ 429
 DB 421 FHGPRGHMMWMDSRLEFNYSWEVLRFLSNARWLEBYKDFRPGDVTSMYTHGLQ 480
 QY 430 MFTGTNGEYFGRTVDVAVYVLMVNDLHGHPDAVSGEDVSGMPTFCIPVDDGVG 489
 DB 481 MFTGTNGEYFGRTVDVAVYVLMVNDLHGHPDAVSGEDVSGMPTFCIPVDDGVG 540
 QY 490 FDRLEMAVADKMTIELKQSDSKMGDIYHTLTNRKMLEKCVTAESHDQALVADKITA 549
 DB 541 FDRLEMAVADKMTIELKQSDSKMGDIYHTLTNRKMLEKCVTAESHDQALVADKITA 600
 QY 550 FWLMDKMDYDPMALDRPSTPRIDGIALHKMIRLVTMGLGEGYLNFNGNEFGHEWIDF 609
 DB 601 FWLMDKMDYDPMALDRPSTPRIDGIALHKMIRLVTMGLGEGYLNFNGNEFGHEWIDF 660
 QY 610 PRPGQTLPTGKVLPGNNNSYDKCRRRPDLGDADFLRYHGMQEPQAMHLEKXGEMTSE 669
 DB 661 PRPGQTLPTGKVLPGNNNSYDKCRRRPDLGDADFLRYHGMQEPQAMHLEKXGEMTSE 720
 QY 670 HQVSRGHEEDKVIIFERGLVFNFNFMWSNFFDYRGCSRPQKXKALDSDDALFGGF 729
 DB 721 HQVSRGHEEDKVIIFERGLVFNFNFMWSNFFDYRGCSRPQKXKALDSDDALFGGF 780
 QY 730 SRLDHDVYFTTEHPHNDNRRSFSVYTPSRATVAYALTE 768
 DB 781 SRLDHDVYFTTEHPHNDNRRSFSVYTPSRATVAYALTE 819

RESULT 5
 09ZTB7 PRELIMINARY; PRT; 734 AA.
 AC 09ZTB7;
 DT 01-MAY-1999 (Tremblrel. 10. Created)
 DT 01-MAY-1999 (Tremblrel. 10. Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25. Last annotation update)
 DE Starch branching enzyme IIA (EC 2.4.1.18).
 GN SBE1 OR SBE1IA.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 OC Triticeae; Hordeum.
 OC NCBI Taxid=4513;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. BOMI;
 RX MEDLINE=8404232; PubMed=9733524;
 RA Sun C., Sathish P., Ahlstrandberg S., Jansson C.;
 RT "The two genes encoding starch-branching enzymes Iia and Iib are
 differentially expressed in barley.";
 RI Plant Physiol. 118:37-49 (1999).
 R EMBL: AF064560; AAC69753.1; -

DR EMBL: AF064562; AAC72335.1; -
 DR GO: GO:0003844; F:1.4-alpha-glucan branching enzyme activity; IEA.
 DR GO: GO:0004556; F:alpha-amylase activity; IEA.
 DR GO: GO:0004555; F:hydrolyase activity, hydrolyzing O-glycosyl. . .; IEA.
 DR GO: GO:0016757; F:transferrase activity, transferring glycosyl. . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR004193; Glyco_hydro_13N.
 DR InterPro: IPR007110; Ig_1ike.
 DR Pfam: PF00128; alpha-amy1ase; 1.
 DR Pfam: PF02922; isoamylase; 1.
 DR GlycoSy:1transferrase; Transferrase.
 SQ SEQUENCE 734 AA; 83832 MW; DE4F0EEDB0ACAF93 CRC64;

Query Match 94.4%; Score 3937; DB 10; Length 724;
 Best Local Similarity 98.5%; Pred. No. 4.6e-286;
 Matches 722; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

36 AEVNTGGAETKLESESEPTQGIYETITDGTGKVELVWGEKPRVVPKPDGQKIYEIDP 95
 2 AEVNTGGAETKLESESEPTQGIYETITDGTGKVELVWGEKPRVVPKPDGQKIYEIDP 61
 96 TKDFRSHLDYRYSRRIIRAIDHEGGLNFSRGYEKLGFTRSAGITIREWAPGASH 155
 62 TKDFRSHLDYRYSRRIIRAIDHEGGLNFSRGYEKLGFTRSAGITIREWAPGASH 121
 156 AALVGDENNMMNPADITMRDVGWEIPLPNNADGSPALPHGSRVKIRMDTPSGVKOSIS 215
 122 AALVGDENNMMNPADITMRDVGWEIPLPNNADGSPALPHGSRVKIRMDTPSGVKOSIS 181
 216 AMIKFSVQAPGEIPNGIYDPEEKKYVQHPQPKRPESLRIYESHIGMSPEPKINSY 275
 182 AMIKFSVQAPGEIPNGIYDPEEKKYVQHPQPKRPESLRIYESHIGMSPEPKINSY 241
 276 ANFRDEVLPRIKRGYNAVQIALQESHYASFGYHVTNFPAPSSRGTPEDLSLIDRA 335
 242 ANFRDEVLPRIKRGYNAVQIALQESHYASFGYHVTNFPAPSSRGTPEDLSLIDRA 301
 336 HELGLVMDIVSHSSNNITDGLNGFGDTTHYFHGPRGHMMWMDSRLEFNYSWEVLR 395
 302 HELGLVMDIVSHSSNNITDGLNGFGDTTHYFHGPRGHMMWMDSRLEFNYSWEVLR 361
 396 FLISNARWLEBYKDFRPGDVTSMYTHGLQMTFTGNYGEYFGRTVDVAVYVLMV 455
 362 FLISNARWLEBYKDFRPGDVTSMYTHGLQMTFTGNYGEYFGRTVDVAVYVLMV 421
 456 NDILHGHPDAVSGEDVSGMPTFCIPVDDGVGFDYRLMAVADKMTIELKQSDSKM 515
 422 NDILHGHPDAVSGEDVSGMPTFCIPVDDGVGFDYRLMAVADKMTIELKQSDSKM 481
 516 GDIVHTLTNRKMLEKCVTAESHDQALVGDKTAFMLMDKMDYDPMALDRPSTPRIDGI 575
 482 GDIVHTLTNRKMLEKCVTAESHDQALVGDKTAFMLMDKMDYDPMALDRPSTPRIDGI 541
 576 ALHKMIRLVTMGLGEGYLNFNGNEFGHEWIDFPRPGQTLPTGKVLPGNNNSYDKCRRR 635
 542 ALHKMIRLVTMGLGEGYLNFNGNEFGHEWIDFPRPGQTLPTGKVLPGNNNSYDKCRRR 601
 636 FDIADADFLRYHGMQEPQAMHLEKXGEMTSEHQVSRGHEEDKVIIFERGLVFN 695
 602 FDIADADFLRYHGMQEPQAMHLEKXGEMTSEHQVSRGHEEDKVIIFERGLVFN 661
 696 FHMWSNFFDYRGCSRPQKXKALDSDDALFGGFSRLDHDVYFTTEHPHNDNRRSFSVY 755
 662 FHMWSNFFDYRGCSRPQKXKALDSDDALFGGFSRLDHDVYFTTEHPHNDNRRSFSVY 721
 756 TFSRTAVVAYALTE 768
 722 TFSRTAVVAYALTE 734

RESULT 6
 024397


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DB      383 HTNFPAPSSRFPTEDLSKLIDKAHELGLVLMVDIVSHASNNLTDLGNGFDGTDTHYF 442
QY      371 HGGPRHHMMWDRSLFNYGSMEVLRFLLSNARWMLLESEYKEDGFRFDGVTSMYTHHGLQM 430
DB      443 HGGPRHHMMWDRSLFNYGSMEVLRFLLSNARWMLLESEYKEDGFRFDGVTSMYTHHGLQV 502
QY      431 TPTGNYGEYFGFATDVAVYVLMVNDLHGLHDAVSIGEDVGMPFCLIPYDDGGYGF 490
DB      503 AFTGNYGEYFGFATDVAVYVLMVNDLHGLHDAVSIGEDVGMPFCLIPYDDGGYGF 562
QY      491 DYRLHMAVADKMIELKQSDSESMWKGDIIVHTLITRRMLEKCVTAESHDQALVGDKTIAF 550
DB      563 DYRLHMAVADKMIELKQSDSESMWKGDIIVHTLITRRMLEKCVTAESHDQALVGDKTIAF 622
QY      551 WLMDCMYDPMALDRPSTPRIDRGIALHKMIRLVTMGIGGEGYINFMGNEFGHEMIDFP 610
DB      623 WLMDCMYDPMALDRPSTPRIDRGIALHKMIRLVTMGIGGEGYINFMGNEFGHEMIDFP 682
QY      611 RGPQTLPTGKVLPGNNNSYDKCRRRFDLGADFLRYHGMQFPDQAMQHLSEKYGMTSEH 670
DB      683 RGPQSLPNSGVLPNNNSYDKCRRRFDLGADFLRYHGMQFPDQAMQHLSEKYGMTSEH 742
QY      671 QYISRKHEEKVLIIFERGDIVFVFNPMKNSFPDYRVGCSRPGRYKVALDSDALFGGFS 730
DB      743 QYISRKHEEKVLIIFERGDIVFVFNPMKNSFPDYRVGCSRPGRYKVALDSDALFGGFS 802
QY      731 RLHDVDVYFTTEHPDNRPRSFVSYYTSPRTAVYALTE 768
DB      803 RLHDVAEYFTADWPHDNRPCSFVYTPRTAVYALTE 840

RESULT 8
ID      024421 PRELIMINARY; PRT: 814 AA.
AC      024421;
DT      01-JAN-1998 (TREMBlrel. 05, Created)
DT      01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT      01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE      Search branching enzyme Ila (EC 2.4.1.18) (Fragment).
GN      SBE2A.
OS      Zea mays (Maize).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      PACCAD clade; Panicoidae; Andropogoneae; Zea.
CX      NCBI_Taxid=4577;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=B73;
RX      MEDLINE=97303618; PubMed=9159942;
RA      Gao M., Fisher D.K., Kim K.N., Shannon J.C., Gultinan M.J.;
RT      "Independent genetic control of maize starch-branching enzymes Ila and
RT      I1b. Isolation and characterization of a Sbe2a cDNA."
RL      Plant Physiol. 114:69-78(1997).
DR      EMBL; U65948; AAC67316.1; -.
DR      PIR; T02041; T02041.
DR      GO; GO:0003844; F.1.4-alpha-glucan branching enzyme activity; IEA.
DR      GO; GO:0004556; F.alpha-amylase activity; IEA.
DR      GO; GO:0004553; F.hydrolyase activity, hydrolyzing O-glycosyl. . .; IEA.
DR      GO; GO:0016757; F.transferase activity, transferring glycosyl. . .; IEA.
DR      InterPro; IPR006047; Alpha_amyl_cat.
DR      InterPro; IPR004193; Glyco_hydro_13N.
DR      Pfam; PF00128; alpha-amylase; 1.
DR      Pfam; PF02922; isoamylase N; 1.
KM      Glycosyltransferase; Transferase.
FT      NON_TER
SQ      SEQUENCE 814 AA; 91866 MW; 0C88B78127511938 CRC64;

Query Match 86.1%; Score 3588.5; DB 10; Length 814;
Best Local Similarity 84.7%; Pred. No. 7e-260;
Matches 662; Conservative 32; Mismatches 49; Indels 39; Gaps 4;

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QY      11 LGVAPPAAPPEELQIEDIEEQTAEVNMTGTAIEKLESSEPTQ----- 55
DB      38 LSAPFPVDTQPEELQIE-----AEL-----TYEK-TSSSPTQTTSAAVAASGVAE 85
QY      56 -----GIYETTTDGTGKVKELVGEKPRVVPKPGGQKTYEIDPLKDRSH 103
DB      86 ERPELSEYVIGVGTTGTTKIDGAKAPALVEKEPVVIPPGGQRIYELDPMLEGRH 145
QY      104 LDYRSEYRIRRAAIDQHEGGLAAPSRYEKGTFTSAEGITREMAFGAHSALVDFN 163
DB      146 LDYRSEYRIRRAAIDQHEGGLAAPSRYEKGTFTSAEGITREMAFGAHSALVDFN 205
QY      164 MNPNPADTMTBDYGVWEIIFLPNNADGSPAIPHGSYKIRMDTPSGYKOSISAWIKSVQ 223
DB      206 MNPNPADMAARNEYGWEIFLPNNADGSPAIPHGSYKIRMDTPSGYKOSIPAWIKSVQ 265
QY      224 APGEIPENGIYYDPPBEKXYVQHPPKRPESIRITYESHIGWSPBEKINSYANFREVL 283
DB      266 APGEIPENGIYYDPPBEKXYVQHPPKRPESIRITYESHIGWSPBEKINTYANFREVL 325
QY      284 PRKELGVNAVOIMAIQESHYSYASFGYHYTNFPAPSSRFPTEDLSKLIDRAHELGLVL 343
DB      326 PRKELGVNAVOIMAIQESHYSYASFGYHYTNFPAPSSRFPTEDLSKLIDRAHELGLVL 385
QY      344 MDIVSHSSNNLTDLGNGFDGTDTHYFHGGPRGHMMWDRSLFNYGSMEVLRFLLSNARW 403
DB      366 MDIVSHSSNNLTDLGNGFDGTDTHYFHGGPRGHMMWDRSLFNYGSMEVLRFLLSNARW 445
QY      404 WLEBYKEDFRPDGVTSMYTHHGLQMTPTGNYGEYFGFATDVAVYVLMVNDLHGLH 463
DB      446 WLEBYKEDFRPDGVTSMYTHHGLQMTPTGNYGEYFGFATDVAVYVLMVNDLHGLH 505
QY      464 PDAVSTIGEDVSGMPTCIPYDDGGYGFYRLHMAVADKMIELKQSDSESMWKGDIIVHTLT 523
DB      506 PDAVSTIGEDVSGMPTCIPYDDGGYGFYRLHMAVADKMIELKQSDSESMWKGDIIVHTLT 565
QY      524 NRRMLEKCVTAESHDQALVGDKTIAFWLMDCMYDPMALDRPSTPRIDRGIALHKMIRL 583
DB      566 NRRMLEKCVTAESHDQALVGDKTIAFWLMDCMYDPMALDRPSTPRIDRGIALHKMIRL 625
QY      584 VTMGIGGEGYINFMGNEFGHEMIDFPGRGQTLPTGKVLPGNNNSYDKCRRRFDLGADY 643
DB      626 VTMGIGGEGYINFMGNEFGHEMIDFPGRGQTLPTGKVLPGNNNSYDKCRRRFDLGADY 685
QY      644 LRHGMQEPDQAMQHLSEKYGMTSEHQYYSRKHEEDKVIIFERGDIVFVFNHMSNGFF 703
DB      686 LRHGMQEPDQAMQHLSEKYGMTSEHQYYSRKHEEDKVIIFERGDIVFVFNHMSNGFF 745
QY      704 DYRVGCSRPGRYKVALDSDALFGGFSRLHDVDVYFTTEHPDNRPRSFVYTPRTAVY 763
DB      746 DYRVGCSRPGRYKVALDSDALFGGFSRLHDVDVYFTTEHPDNRPRSFVYTPRTAVY 805
QY      764 YA 765
DB      806 YA 807

RESULT 9
ID      040663 PRELIMINARY; PRT: 825 AA.
AC      040663;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE      Branching enzyme-3 precursor.
OS      Oryza sativa (Rice).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzae; Oryza.
CX      NCBI_Taxid=4530;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=93366833; PubMed=8360192;

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DB 535 DKMIEFLKOSDEAMKMGDIHTLTNRRLKCVTAESHQALVGDKTIAFWLMDKMD 594
QY 560 FMALDPRSTPRIDRGIALHNMIRLVTVGLGEGYLTNFMNGEFGHPREWIDPRGQTLPTG 619
DB 595 FMALDPRPTITIDRGIALHNMIRLTGGLGEGYLTNFMNGEFGHPREWIDPRGQTLPTG 654
QY 620 KYLPNNNSYDKCRRRFDLGDADLRYHGMQEFQANQHLBEKXGPMISEHQYSRKHEE 679
DB 655 KFIPIGNNSYDKCRRRFDLGDADLRYHGMQEFQANQHLBEKXGPMISEHQYSRKHEE 714
QY 680 DKITIFERGLVVFENFMHNSFEFDYVGSRGPKYKVALDSDALFGSGFRLDHDVDF 739
DB 715 DKMIEFGDLVVFENFMHNSFEFDYVGSRGPKYKVALDSDALFGSGFRLDHDVDF 774
QY 740 TTEPHDNRRPSFSVTPSPRTAVVYALTE 768
DB 775 TTDSHNRPSFSVTPSPRTAVVYALTE 803

RESULT 11
ID 081387 PRELIMINARY; PRT; 799 AA.
AC 081387;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Search branching enzyme IIB.
GN Zea mays (Maize).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxId=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Kim K.-N., Fisher D.K., Gao M., Guitman M.J.;
RT "Molecular cloning and characterization of the amylose-extender gene
RT encoding starch branching enzyme IIB in maize."
RT Submitted (JUN-1998) to the EMBL/Genbank/DBD databases.
RL
DR EMBL, AF072725; AAC33764.1; -.
DR PIR, T01663; T01663.
DR GO, GO:0004556; F:alpha-amylose activity; IEA.
DR GO, GO:0005507; F:copper ion binding; IEA.
DR GO, GO:0005489; F:electron transporter activity; IEA.
DR GO, GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO, GO:0005975; P:carbohydrate metabolism; IEA.
DR GO, GO:0006118; P:electron transport; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR000923; Alpha_amy1.
DR InterPro: IPR004193; Glyco_hydro_13N.
DR Pfam: PF00128; alpha-amylose; 1.
DR Pfam: PF02922; isoamylose_N; 1.
DR PROSITE, PS00196; COPPER_BLUE; 1.
SQ SEQUENCE 799 AA; 90665 MW; 4FD7B1BC3B759F0 CRC64;

Query Match 80.4%; Score 3351; DB 10; Length 799;
Best Local Similarity 78.5%; Pred. No. 4,3e-242;
Matches 609; Conservative 68; Mismatches 77; Indels 22; Gaps 4;

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QY 173 TRDVGWEIFLNNADGSPALPHGSRVKIRMDTSGVSDISAMIKFSVQAGELIPNG 232
DB 204 SKNERGVWEIFLNNADGSPALPHGSRVKIRMDTSGVSDISAMIKFSVQAGELIPNG 263
QY 223 IYDPEEKEKYVFOHPQKRPESLRNYESHIGKSSPEPKINSYANRDEVLPTIKRLQYN 292
DB 264 IYDPEEKEKYVFOHPQKRPESLRNYESHIGKSSPEPKINSYANRDEVLPTIKRLQYN 323
QY 293 AVQIALIGHSYYAARGYVTVTFPAASSRFGPREDKSLIDRAHEGLVLMIVHSSS 352
DB 324 AVQIALIGHSYYAARGYVTVTFPAASSRFGPREDKSLIDRAHEGLVLMIVHSSS 383
QY 363 NNTLDGLNFGDGLDTHYFHGSPRGHMMDSRLFNYSMEVLRFLSNARWLEBYKFDG 412
DB 384 NNTLDGLNFGDGLDTHYFHGSPRGHMMDSRLFNYSMEVLRFLSNARWLEBYKFDG 443
QY 413 PRFDGVTSMYTHHGLQMTFTGNYGEYFGFATDVAVYIAMLVNDLHGHPDAVSGED 472
DB 444 PRFDGVTSMYTHHGLQMTFTGNYGEYFGFATDVAVYIAMLVNDLHGHPDAVSGED 503
QY 473 VSGMPTFCIPVDPGGVGFYRMMAVADKWIILKOSDESKMGDIHTLTNRRLKCV 532
DB 504 VSGMPTFCIPVDPGGVGFYRMMAVADKWIILKOSDESKMGDIHTLTNRRLKCV 563
QY 533 TYAESHQALVGDKTIAFWLMDKMDYFMALDPRSTPRIDRGIALHNMIRLVTVGLGEG 592
DB 564 TYAESHQALVGDKTIAFWLMDKMDYFMALDPRSTPRIDRGIALHNMIRLVTVGLGEG 623
QY 593 YLNFMGNEGRHPEWIDPRGQTLPTGKVLPGNNNSYDKCRRRFDLGDADLRYHGMQEF 652
DB 624 YLNFMGNEGRHPEWIDPRGQTLPTGKVLPGNNNSYDKCRRRFDLGDADLRYHGMQEF 683
QY 653 DQMOHLEBKXGPMISEHQYSRKHEEKYIIFERGLVVFENFMHNSFEFDYVGSRG 712
DB 684 DQMOHLEBKXGPMISEHQYSRKHEEKYIIFERGLVVFENFMHNSFEFDYVGSRG 743
QY 713 GKRYKVALDSDALFGSGFRLDHDVDFTEPHDNRRPSFSVTPSPRTAVVYALTE 768
DB 744 GKRYKVALDSDALFGSGFRLDHDVDFTEPHDNRRPSFSVTPSPRTAVVYALTE 803

RESULT 12
ID 092786 PRELIMINARY; PRT; 829 AA.
AC 092786;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Search branching enzyme IIB.
GN SBE1 OR SBE1B.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxId=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. BOM1;
RA Sun C., Sathish P., Ahlstrandberg S., Jansson C.;
RT "The two genes encoding starch-branching enzymes IIA and IIB are
RT differentially expressed in barley."
RL Plant Physiol. 118:37-49 (1998).
DR EMBL, AF064561; AAC69754.1; -.
DR EMBL, AF064563; AAC72336.1; -.
DR GO, GO:0004556; F:alpha-amylose activity; IEA.
DR GO, GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO, GO:0016757; F:transferase activity, transferring glycosyl . . .; IEA.
DR GO, GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR004193; Glyco_hydro_13N.
DR Pfam: PF00128; alpha-amylose; 1.
DR Pfam: PF02922; isoamylose_N; 1.

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Db 722 LRYHGMQEPFRAMQHLERXYGFMTESEHQYISRKNEGDVILIFERDNLVFNFEHMTNSYS 781
QY 704 DYXVGCSPGPKYKXVALSDDLFGGFSRLDDVDVFTTEHPHNDNPRGFSVYTPRTAVY 763
Db 782 DYXVGCSPGPKYKXVALSDDLFGGFSRLDDVDVFTTEHPHNDNPRGFSVYTPRTAVY 841
QY 764 YALTE 768
Db 842 YALAD 846

RESULT 14
QXISS PRELIMINARY; PRT; 870 AA.
AC 09XISS;
DB 01-NOV-1999 (TReMBLrel. 12, Created)
DB 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DB 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DB Branching enzyme 1 precursor (EC 2.4.1.18).
KBE1.
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
NCBI_TaxId=3885;
RN [1]
RP SEQUENCE FROM N.A.
RA Nozaki K., Ito H., Matsui H., Honma M.;
RT "Phaseolus vulgaris L. mRNA for starch branching enzyme 1.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029548; BAA82348.1; -
DR GO; GO:0003844; F:1.4-alpha-glucan branching enzyme activity; IEA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity; hydrolyzing O-glycosyl. . .; IEA.
DR GO; GO:0016757; F:transferase activity; transferring glycosyl. . .; IEA.
DR InterPro; IPR006047; P:carbohydrate metabolism; IEA.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02922; isoamylase_N; 1.
DR GlycoStyl; GlycoStyl; Transferrase; Transferrase; Transferrase.
KW TRANSIT 1 156 POTENTIAL.
SQ SEQUENCE 870 AA; 98891 MW; BDB5C028B6694EC CRC64;

Query Match 79.3%; Score 3307.5; DB 10; Length 870;
Best Local Similarity 76.3%; Pred. No. 8.9e-235;
Matches 601; Conservative 72; Mismatches 78; Indels 37; Gaps 4;

QY 18 AAAPEELQIPED-----IEBQTAENVMTGTAEKLE-----SSAPTQGIIVT-----I 61
Db 58 AIAESDKVLPQDDHNSASLTQDETPITVSANDLMDLMDMDKXNIGADSSYXQI 117
QY 62 TDG-----VTGKVELVGEKRPVVPKPDGQKTIYDPTLKD 100
Db 118 EDGGSVASSPVDVDPKAKTSVSQGEVKIPSVAKPKKIIIPRPAQGKTIYDIDSLAY 177
QY 101 RSHLDYVSEKRRRAALDQHEGGLAASRGYKGFIRSAEGITTYREKAPAHSAALVG 160
Db 178 RDHLDFRFGQYRIADHETINKHEGGIDAKSRGEGFIRSAAGITTYREKAPAHSAALVG 237
QY 161 DFNMMNADTMETDDYGVMEIFLPNNADGSPAIHGRGVKIRMDTPSGVKDSISAMIXF 220
Db 238 DFNMMNADTMETDDYGVMEIFLPNNADGSPAIHGRGVKIRMDTPSGVKDSISAMIXF 297
QY 221 SVQAPGEIPFNGIYDPEEEKYVFOHPQKPSLRITYESHIGSSPEPKNSYANFSD 280
Db 298 SVQAPGEIPFNGIYDPEEEKYVFOHPQKPSLRITYESHIGSSPEPKNSYANFSD 357
QY 261 EVLRIRKLGNAVOIMAIOESHYASFGYVNTNFFASRSRGTEDDLKSLIDRAHEGL 340
Db 358 DVLPRIKLGNNAVOIMAIOESHYASFGYVNTNFFASRSRGTEDDLKSLIDRAHEGL 417

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QY 341 LVLMIDIVSHSSNNLTDLGNGFDGDTIDHYFHGGPRGHMMWDSRLFNYSWEVIRFLSN 400
Db 418 LVLMIDIVSHSSNNLTDLGNGFDGDTIDHYFHGGPRGHMMWDSRLFNYSWEVIRFLSN 477
QY 401 ARWLEERYKFDGRFPGVTSMTYTHGLQMTFTGNIGYEGFADVDVAVYVLMVNDLIH 460
Db 478 ARWLEERYKFDGRFPGVTSMTYTHGLQMTFTGNIGYEGFADVDVAVYVLMVNDLIH 537
QY 461 GLHPDAVSIQEDVSGMPTFCIPVDDGVGFYDLHMAVAWKIETLKOSDSMMKGDIVH 520
Db 538 GLHPDAVSIQEDVSGMPTFCIPVDDGVGFYDLHMAVAWKIETLKOSDSMMKGDIVH 597
QY 521 TLNRRMLEKCVTYAESHQALVGDKTIAFWLMDKMDYDPMALDRPSTPRIDRGIATLHKM 580
Db 598 TLNRRMLEKCVTYAESHQALVGDKTIAFWLMDKMDYDPMALDRPSTPRIDRGIATLHKM 657
QY 581 IRLVTMLGEGYGLNNGNEFGHPENIDFPRGQTLPTGKYLPGNNNSYDKCRERFDLGD 640
Db 658 IRLVTMLGEGYGLNNGNEFGHPENIDFPRGQTLPTGKYLPGNNNSYDKCRERFDLGD 717
QY 641 ADFLRXHGQEPDQANQLEKYGFMTESEHQYISRKNEGDVILIFERDNLVFNFEHMTNS 700
Db 718 ADFLRXHGQEPDQANQLEKYGFMTESEHQYISRKNEGDVILIFERDNLVFNFEHMTNS 777
QY 701 SFEDYVVGSRPCKYKXVALSDDLFGGFSRLDDVDVFTTEHPHNDNPRGFSVYTPRT 760
Db 778 SFEDYVVGSRPCKYKXVALSDDLFGGFSRLDDVDVFTTEHPHNDNPRGFSVYTPRT 837
QY 761 YALTE 768
Db 838 YALAD 845

RESULT 15
QXISS PRELIMINARY; PRT; 800 AA.
AC 042531;
DB 01-NOV-1996 (TReMBLrel. 01, Created)
DB 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DB 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DB Starch branching enzyme class II (EC 2.4.1.18) (fragment).
DE SBE2-2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxId=702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ecotype Columbia; TISSUE=Hypocotyl;
RX MEDLINE=96197401; PubMed=8616246;
RA Fisher D.K., Gao M., Kim K.N., Boyer C.D., Gullitman M.J.;
RT "Two closely related cDNAs encoding starch branching enzyme from
Arabidopsis thaliana."
RT Plant Mol. Biol. 30:97-108 (1996).
RL EMBL; U22428; AAB03100.1; -
DR PIR; S65046; S65046.
DR GO; GO:0003844; F:1.4-alpha-glucan branching enzyme activity; IEA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity; hydrolyzing O-glycosyl. . .; IEA.
DR GO; GO:0016757; F:transferase activity; transferring glycosyl. . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02922; isoamylase_N; 1.
DR GlycoStyl; GlycoStyl; Transferrase; Transferrase.
KW NON TER 1
SQ SEQUENCE 800 AA; 92098 MW; 8D47E940B403258 CRC64;

Query Match 78.1%; Score 3258; DB 10; Length 800;
Best Local Similarity 76.6%; Pred. No. 4e-235;
Matches 584; Conservative 75; Mismatches 71; Indels 32; Gaps 4;

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QY 18 AAAQPELQIPE-----DIEQTAENVMTGGTAELKESSEPTQIIVETITDG 64
DB 54 AIBASEKVLVPDNLDDDDPRGFSQIFLESQIMEX-----TEAVRTEDQIMNV----- 100
QY 65 VIKGYVELVVGKPRVYKPGDQOKIYEIDPTLKDPRSHLDYRYSEKRIIRAIDQHEGG 124
DB 101 ---VKER--GVKPRIVPPDGDGKIYEIDPMLRTYNNHLDYRYQYKRLREIDKXEGG 154
QY 125 LEAFSGYEXLGTFRSAEGITTYREMAPASALVGDENNPNPADTWTTRDDYGVWEIFL 184
DB 155 LEAFSGYEXLGTFRSAGITTYREMAPAKAASLIGDENNNNSNADITRNEFGVWEIFL 214
QY 185 PNNADGSPALPHGSRVYKIMDTPSGVXDSISAMIKFSVQAPGEIIPNGIYYDPPEEKYV 244
DB 215 PNNTDGSPALPHGSRVYKIMDTPSGIKDSIPAWIKFSVQAPGEIIPNGIYYDPPEEKYV 274
QY 245 FQHPQKRPESLRIYESHIGMSPEPKINSYANFRDEVLPRIKLGYNVQIMAIQESHY 304
DB 275 FQHPQKRPESLRIYESHIGMSPEPKINSYANFRDEVLPRIKLGYNVQIMAIQESHY 334
QY 305 YASFGYHVTTFPAPSSRFGTPEDLKSLIDRAHEGLVLMIDIVSHSSNNTLDDGLNGFDG 364
DB 335 YASFGYHVTTFPAPSSRFGTPEDLKSLIDRAHEGLVLMIDIVSHSSNNTLDDGLNGFDG 394
QY 365 TDTHYFHGGRGHMMWMDSLFNYGSWEVLRFLSNARWMLBXYKFDGFRPDGYTSMYT 424
DB 395 TDHAYFHSGRGVHMMWMDSLFNYGSWEVLRFLSNARWMLBXYKFDGFRPDGYTSMYT 454
QY 425 HHGLQMTFTGNIGEYGFATDVDAVYLMVNDLIHGLHPDAVSGEDVSGMPTFCIPV 484
DB 455 HHGLSYGFTGNITEYGFLETDVDAVYLMVNDMIHGLYPEALITVGEDEVSGMPTFCIPVQ 514
QY 485 DGGVGFYDLHMAVADKMIELLKQSDSWMKGDIVHTLTNRMTLEKCVTAESHDAQLVG 544
DB 515 DGGVGFYDLHMAVADKMIELLKQSDSWMKGDIVHTLTNRMTLEKCVTAESHDAQLVG 574
QY 545 DKTIAFWLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVMTGLGEGYINFMGNFQHP 604
DB 575 DKTIAFWLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVMTGLGEGYINFMGNFQHP 634
QY 605 EMTDPRGPGTLETKYLPENNNNSYDKCRRRFDLGDADFLRYHGOEFQDQMOHLEEKY 664
DB 635 EMTDPRGPGTLETKYLPENNNNSYDKCRRRFDLGDADFLRYHGOEFQDQMOHLEEKY 694
QY 665 FMTSEHQYVSRKAEEDKVIIFERGDVLFVFNFMHNSFPDYRVGCSRPGKYKVALDSDDA 724
DB 695 FMTSEHQYVSRKAEEDKVIIFERGDVLFVFNFMHNSFPDYRVGCSRPGKYKVALDSDDA 754
QY 725 LFGGFSRLDHDVDYFTTEHPHNDKPRGFSYTPGRTAVVYAL 766
DB 755 LFGGFSRLDHDVDYFTTEHPHNDKPRGFSYTPGRTAVVYAL 796
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Search completed: April 15, 2004, 08:38:09
Job time : 56 secs